

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lin, Lih-Ling
Chen, Jennifer H.
Schievella, Andrea
Graham, James

(ii) TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND PROTEINS AND INHIBITORS OF LIGAND BINDING

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 Cambridge Park Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.
(B) REGISTRATION NUMBER: 32,724
(C) REFERENCE/DOCKET NUMBER: GI5232D

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..1231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

C AGC AAT GCA GGT GAT GGA CCA GGT GGC GAG GGC AGT GTT CAC CTG
Ser Asn Ala Gly Asp Gly Pro Gly Gly Gly Ser Val His Leu
1 5 10 15

15

GCA AGC TCT CGG GGC ACT TTG TCT GAT AGT GAA ATT GAG ACC AAC TCT Ala Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile Glu Thr Asn Ser 20 25 30	94
GCC ACA AGC ACC ATC TTT GGT AAA GCC CAC AGC TTG AAG CCA AGC ATA Ala Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile 35 40 45	142
AAG GAG AAG CTG GCA GGC AGC CCC ATT CGT ACT TCT GAA GAT GTG AGC Lys Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser 50 55 60	190
CAG CGA GTC TAT CTC TAT GAG GGA CTC CTA GGC AAA GAG CGT TCT ACT Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr 65 70 75	238
TTA TGG GAC CAA ATG CAA TTC TGG GAA GAT GCC TTC TTA GAT GCT GTG Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val 80 85 90 95	286
ATG TTG GAG AGA GAA GGG ATG GGT ATG GAC CAG GGT CCC CAG GAA ATG Met Leu Glu Arg Glu Gly Met Gly Asp Gln Gly Pro Gln Glu Met 100 105 110	334
ATC GAC AGG TAC CTG TCC CTT GGA GAA CAT GAC CGG AAG CGC CTG GAA Ile Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu 115 120 125	382
GAT GAT GAA GAT CGC TTG CTG GCC ACA CTT CTG CAC AAC CTC ATC TCC Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser 130 135 140	430
TAC ATG CTG CTG ATG AAG GTA AAT AAG AAT GAC ATC CGC AAG AAG GTG Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val 145 150 155	478
AGG CGC CTA ATG GGA AAG TCG CAC ATT GGG CTT GTG TAC AGC CAG CAA Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln 160 165 170 175	526
ATC AAT GAG GTG CTT GAT CAG CTG GCG AAC CTG AAT GGA CGC GAT CTC Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu 180 185 190	574
TCT ATC TGG TCC AGT GGC AGC CGG CAC ATG AAG AAG CAG ACA TTT GTG Ser Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val 195 200 205	622
GTA CAT GCA GGG ACA GAT ACA AAC GGA GAT ATC TTT TTC ATG GAG GTG Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val 210 215 220	670
TGC GAT GAC TGT GTG TTG CGT AGT AAC ATC GGA ACA GTG TAT GAG Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu 225 230 235	718
CGC TGG TGG TAC GAG AAG CTC ATC AAC ATG ACC TAC TGT CCC AAG ACG Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr 240 245 250 255	766
AAG GTG TTG TGC TTG TGG CGT AGA AAT GGC TCT GAG ACC CAG CTC AAC Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn 260 265 270	814

DRAFT 3/6/2004

AAG TTC TAT ACT AAA AAG TGT CGG GAG CTG TAC TAC TGT GTG AAG GAC Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp 275 280 285	862
AGC ATG GAG CGC GCT GCC CGA CAG CAA AGC ATC AAA CCC GGA CCT Ser Met Glu Arg Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro 290 295 300	910
GAA TTG GGT GGC GAG TTC CCT GTG CAG GAC CTG AAG ACT GGT GAG GGT Glu Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly 305 310 315	958
GGC CTG CTG CAG GTG ACC CTG GAA GGG ATC AAC CTC AAA TTC ATG CAC Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His 320 325 330 335	1006
AAT CAG GTT TTC ATA GAG CTG AAT CAC ATT AAA AAG TGC AAT ACA GTT Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val 340 345 350	1054
CGA GGC GTC TTT GTC CTG GAG GAA TTT GTT CCT GAA ATT AAA GAA GTG Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val 355 360 365	1102
G TG AGC CAC AAG TAC AAG ACA CCA ATG GCC CAC GAA ATC TGC TAC TCC Val Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser 370 375 380	1150
GTA TTA TGT CTC TTC TCG TAC GTG GCT GCA GTT CAT AGC AGT GAG GAA Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu 385 390 395	1198
GAT CTC AGA ACC CCG CCC CGG CCT GTC TCT AGC TGATGGAGAG GGGCTACGCA Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser 400 405 410	1251
GCTGCCAG CCCAGGGCAC GCCCCTGGCC CCTTGCTGTT CCCAAGTGCA CGATGCTGCT	1311
GTGACTGAGG AGTGGATGAT GCTCGTGTGT CCTCTGCAAG CCCCTGCTG TGGCTTGGGT	1371
GGGTACCGGT TATGTGTCCC TCTGAGTGTG TCTTGAGCGT GTCCACCTTC TCCCTCTCCA	1431
CTCCCAGAAG ACCAAACTGC CTTCCCCTCA GGGCTCAAGA ATGTGTACAG TCTGTGGGC	1491
CGGTGTGAAC CCACTATTTT GTGTCCCTGA GACATTGTG TTGTGGTTCC TTGTCCCTGT	1551
CCCTGGCGTT AACTGTCCAC TGCAAGAGTC TGGCTCTCCC TTCTCTGTGA CCCGGCATGA	1611
CTGGGCGCCT GGAGCAGTTT CACTCTGTGA GGAGTGAGGG AACCCCTGGGG CTCACCCCTCT	1671
CAGAGGAAGG GCACAGAGAG GAAGGGAAGA ATTGGGGGGC AGCCGGAGTG AGTGGCAGCC	1731
TCCCTGCTTC CTTCTGCATT CCCAAGCCGG CAGCTACTGC CCAGGGCCCG CAGTGTGGC	1791
TGCTGCCTGC CACAGCCTCT GTGACTGCAG TGGAGCGCG AATTCCCTGT GGCCTGCCAC	1851
GCCTTCGGCA TCAGAGGATG GAGTGGTCGA GGCTAGTGGA GTCCCAGGGA CCGCTGGCTG	1911
CTCTGCCTGA GCATCAGGGA GGGGGCAGGA AAGACCAAGC TGGTTTGCA CATCTGTCTG	1971
CAGGCTGTCT CTCCAGGCAC GGGGTGTCAG GAGGGAGAGA CAGCCTGGGT ATGGGCAAGA	2031
AATGACTGTA AATATTCAG CCCCACATTA TTTATAGAAA ATGTACAGTT GTGTGAATGT	2091
GAAATAATG TCCTCACCTC CCAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	2151
AAAAAAA	2158

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly Ser Val His Leu Ala
1 5 10 15

Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile Glu Thr Asn Ser Ala
20 25 30

Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile Lys
35 40 45

Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser Gln
50 55 60

Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu
65 70 75 80

Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val Met
85 90 95

Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met Ile
100 105 110

Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu Asp
115 120 125

Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser Tyr
130 135 140

Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val Arg
145 150 155 160

Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln Ile
165 170 175

Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser
180 185 190

Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val Val
195 200 205

His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val Cys
210 215 220

Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg
225 230 235 240

Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys
245 250 255

Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys
260 265 270

Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser
275 280 285

7

Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu
 290 295 300

Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly Gly
 305 310 315 320

Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His Asn
 325 330 335

Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val Arg
 340 345 350

Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val Val
 355 360 365

Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser Val
 370 375 380

Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu Asp
 385 390 395 400

Leu Arg Thr Pro Pro Arg Pro Val Ser Ser
 405 410

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

G GAG GTG CAG GAC CTC TTC GAA GCC CAG GGC AAT GAC CGA CTG AAG	46
Glu Val Gln Asp Leu Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys	
1 5 10 15	
CTG CTG GTG CTG TAC AGT GGA GAG GAT GAT GAG CTG CTA CAG CGG GCA	94
Leu Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala	
20 25 30	
GCT GCC GGG GGC TTG GCC ATG CTT ACC TCC ATG CGG CCC ACG CTC TGC	142
Ala Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys	
35 40 45	
AGC CGC ATT CCC CAA GTG ACC ACA CAC TGG CTG GAG ATC CTG CAG GCC	190
Ser Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala	
50 55 60	
CTG CTT CTG AGC TCC AAC CAG GAG CTG CAG CAC CGG GGT GCT GTG GTG	238
Leu Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val	
65 70 75	
GTG CTG AAC ATG GTG GAG GCC TCG AGG GAG ATT GCC AGC ACC CTG ATG	286
Val Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met	
80 85 90 95	

7

7

GAG AGT GAG ATG ATG GAG ATC TTG TCA GTG CTA GCT AAG GGT GAC CAC Glu Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His 100 105 110	334
AGC CCT GTC ACA AGG GCT GCT GCA GCC TGC CTG GAC AAA GCA GTG GAA Ser Pro Val Thr Arg Ala Ala Ala Cys Leu Asp Lys Ala Val Glu 115 120 125	382
TAT GGG CTT ATC CAA CCC AAC CAA GAT GGA GAG TGAGGGGTT GTCCCTGGC Tyr Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu 130 135	435
CCAAGGCTCA TGCACACGCT ACCTATTGTG GCACGGAGAG TAAGGACGGA AGCAGCTTG GCTGGTGGTG GCTGGCATGC CCAATACTCT TGCCCATCCT CGCTTGCTGC CCTAGGATGT CCTCTGTTCT GAGTCAGCGG CCACGTTCAAG TCACACAGCC CTGCTTGGCC AGCACTGCCT GCAGCCTCAC TCAGAGGGGC CCTTTTCTG TACTACTGTA GTCAGCTGGG AATGGGAAAG GTGCATCCCA ACACAGCCTG TGATCCTGG GGCATTTGGA AGGGCGCACA CATCAGCAGC CTCACCAAGCT GTGAGCCTGC TATCAGGCCT GCCCCTCCAA TAAAAGTGTG TAGAACTCCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 826	495 555 615 675 735 795

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Val Gln Asp Leu Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys Leu
1 5 10 15

Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala
20 25 30

Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser
35 40 45

Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu
50 55 60 ..

Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val Val
65 70 75 80

Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met Glu
85 90 95

Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His Ser
100 105 110

Pro Val Thr Arg Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr
115 120 125

Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu
130 135

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

G GAG AAG CCG CTG CAC GCC CTG CAC GGC CGC GGG GTT TGC CTC Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu 1 5 10 15	46
AAC GAA AAG AGC TAC CGC GAG CAA GTC AAG ATC GAG AGA GAC TCC CGT Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg 20 25 30	94
GAG CAC GAG GAG CCC ACC ACC TCT GAG ATG GCC GAG GAG ACC TAC TCC Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser 35 40 45	142
CCC AAG ATC TTC CGG CCC AAA CAC ACC CGC ATC TCC GAG CTG AAG GCT Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala 50 55 60	190
GAA GCA GTG AAG AAG GAC CGC AGA AAG AAG CTG ACC CAG TCC AAG TTT Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe 65 70 75	238
GTC GGG GGA GCC GAG AAC ACT GCC CAC CCC CGG ATC ATC TCT GAA CCT Val Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Glu Pro 80 85 90 95	286
GAG ATG AGA CAG GAG TCT GAG CAG GGC CCC TGC CGC AGA CAC ATG GAG Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu 100 105 110	334
GCT TCC CTG CAG GAG CTC AAA GCC AGC CCA CGC ATG GTG CCC CGT GCT Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala 115 120 125	382
GTG TAC CTG CCC AAT TGT GAC CGC AAA GGA TTC TAC AAG AGA AAG CAG Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln 130 135 140	430
TGC AAA CCT TCC CGT GGC CGC AAG CGT GGC ATC TGC TGG TGC GTG GAC Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp 145 150 155	478
AAG TAC GGG ATG AAG CTG CCA GGC ATG GAG TAC GTT GAC GGG GAC TTT Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe 160 165 170 175	526
CAG TGC CAC ACC TTC GAC AGC AGC AAC GTT GAG TGATGCGTCC CCCCCCAACC Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu 180 185	579
TTTCCCTCAC CCCCTTCCAC CCCCAGCCCC GACTCCAGCC AGCGCCTCCC TCCACCCCCAG	639

GACGCCACTC ATTCATCTC ATTTAAGGGA AAAATATATA TCTATCTATT TGAGGAAAAA	699
AAAAAAAAAAA AAAAAAAAAAA AAA	722

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn	
1 5 10 15	
Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu	
20 25 30	
His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro	
35 40 45	
Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu	
50 55 60	
Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val	
65 70 75 80	
Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Glu Pro Glu	
85 90 95	
Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala	
100 105 110	
Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val	
115 120 125	
Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys	
130 135 140	
Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys	
145 150 155 160	
Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln	
165 170 175	
Cys His Thr Phe Asp Ser Ser Asn Val Glu	
180 185	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1023 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 57..875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCTGCACTC TCGCTCTCCT GCCCCACCCC GAGGTAAAGG GGGCGACTAA GAGAAG	56
ATG GTG TTG CTC ACC GCG GTC CTC CTG CTG CTG GCC GCC TAT GCG GGG Met Val Leu Leu Thr Ala Val Leu Leu Leu Ala Ala Tyr Ala Gly	104
1 5 10 15	
CCG GCC CAG AGC CTG GGC TCC TTC GTG CAC TGC GAG CCC TGC GAC GAG Pro Ala Gln Ser Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu	152
20 25 30	
AAA GCC CTC TCC ATG TGC CCC CCC AGC CCC CTG GGC TGC GAG CTG GTC Lys Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val	200
35 40 45	
AAG GAG CCG GGC TGC GGC TGC ATG ACC TGC GCC CTG GGC GAG GGG Lys Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly	248
50 55 60	
CAG TCG TGC GGC GTC TAC ACC GAG CGC TGC GCC CAG GGG CTG CGC TGC Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys	296
65 70 75 80	
CTC CCC CGG CAG GAC GAG AAG CCG CTG CAC GCC CTG CTG CAC GGC Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly	344
85 90 95	
CGC GGG GTT TGC CTC AAC GAA AAG AGC TAC CGC GAG CAA GTC AAG ATC Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile	392
100 105 110	
GAG AGA GAC TCC CGT GAG CAC GAG GAG CCC ACC ACC TCT GAG ATG GCC Glu Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala	440
115 120 125	
GAG GAG ACC TAC TCC CCC AAG ATC TTC CGG CCC AAA CAC ACC CGC ATC Glu Glu Thr Tyr Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile	488
130 135 140	
TCC GAG CTG AAG GCT GAA GCA GTG AAG AAG GAC CGC AGA AAG AAG CTG Ser Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu	536
145 150 155 160	
ACC CAG TCC AAG TTT GTC GGG GGA GCC GAG AAC ACT GCC CAC CCC CGG Thr Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg	584
165 170 175	
ATC ATC TCT GCA CCT GAG ATG AGA CAG GAG TCT GAG CAG GGC CCC TGC Ile Ile Ser Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys	632
180 185 190	
CGC AGA CAC ATG GAG GCT TCC CTG CAG GAG CTC AAA GCC AGC CCA CGC Arg Arg His Met Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg	680
195 200 205	
ATG GTG CCC CGT GCT GTG TAC CTG CCC AAT TGT GAC CGC AAA GGA TTC Met Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe	728
210 215 220	
TAC AAG AGA AAG CAG TGC AAA CCT TCC CGT GGC CGC AAG CGT GGC ATC Tyr Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile	776
225 230 235 240	

TGC TGG TGC GTG GAC AAG TAC GGG ATG AAG CTG CCA GGC ATG GAG TAC Cys Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr 245 250 255	824
GTT GAC GGG GAC TTT CAG TGC CAC ACC TTC GAC AGC AGC AAC GTT GAG Val Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu 260 265 270	872
TGATGCGTCC CCCCCCAACC TTTCCCTCAC CCCCTCCAC CCCCAGCCCC GACTCCAGCC AGCGCCTCCC TCCACCCCCAG GACGCCACTC ATTTCATCTC ATTTAAGGGA AAAATATATA TCTATCTATT TGAAAAAAA AAAAAAAACC C	932
	992
	1023

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Leu Leu Thr Ala Val Leu Leu Leu Ala Ala Tyr Ala Gly 1 5 10 15
Pro Ala Gln Ser Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu 20 25 30
Lys Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val 35 40 45
Lys Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly 50 55 60
Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys 65 70 75 80
Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly 85 90 95
Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile 100 105 110
Glu Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala 115 120 125
Glu Glu Thr Tyr Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile 130 135 140
Ser Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu 145 150 155 160
Thr Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg 165 170 175
Ile Ile Ser Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys 180 185 190
Arg Arg His Met Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg 195 200 205
Met Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe 210 215 220

Tyr Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile
 225 230 235 240
 Cys Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr
 245 250 255
 Val Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
 260 265 270

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1694 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

C TCT CTC AAG GCC AAC ATC CCT GAG GTG GAA GCT GTC CTC AAC ACC	46
Ser Leu Lys Ala Asn Ile Pro Glu Val Ala Val Leu Asn Thr	
1 5 10 15	
GAC AGG AGT TTG GTG TGT GAT GGG AAG AGG GGC TTA TTA ACT CGT CTG	94
Asp Arg Ser Leu Val Cys Asp Gly Lys Arg Gly Leu Leu Thr Arg Leu	
20 25 30	
CTG CAG GTC ATG AAG AAG GAG CCA GCA GAG TCG TCT TTC AGG TTT TGG	142
Leu Gln Val Met Lys Lys Glu Pro Ala Glu Ser Ser Phe Arg Phe Trp	
35 40 45	
CAA GCT CGG GCT GTG GAG AGT TTC CTC CGA GGG ACC ACC TCC TAT GCA	190
Gln Ala Arg Ala Val Glu Ser Phe Leu Arg Gly Thr Thr Ser Tyr Ala	
50 55 60	
GAC CAG ATG TTC CTG CTG AAG CGA GGC CTC TTG GAG CAC ATC CTT TAC	238
Asp Gln Met Phe Leu Leu Lys Arg Gly Leu Leu Glu His Ile Leu Tyr	
65 70 75	
TGC ATT GTG GAC AGC GAG TGT AAG TCA AGG GAT GTG CTC CAG AGT TAC	286
Cys Ile Val Asp Ser Glu Cys Lys Ser Arg Asp Val Leu Gln Ser Tyr	
80 85 90 95	
TTT GAC CTC CTG GGG GAG CTG ATG AAG TTC AAC GTT GAT GCA TTC AAG	334
Phe Asp Leu Leu Gly Glu Leu Met Lys Phe Asn Val Asp Ala Phe Lys	
100 105 110	
AGA TTC AAT AAA TAT ATC AAC ACC GAT GCA AAG TTC CAG GTA TTC CTG	382
Arg Phe Asn Lys Tyr Ile Asn Thr Asp Ala Lys Phe Gln Val Phe Leu	
115 120 125	

AAG CAG ATC AAC AGC TCC CTG GTG GAC TCC AAC ATG CTG GTG CGC TGT 430
 Lys Gln Ile Asn Ser Ser Leu Val Asp Ser Asn Met Leu Val Arg Cys
 130 135 140
 GTC ACT CTG TCC CTG GAC CGA TTT GAA AAC CAG GTG GAT ATG AAA GTT 478
 Val Thr Leu Ser Leu Asp Arg Phe Glu Asn Gln Val Asp Met Lys Val
 145 150 155
 GCC GAG GTA CTG TCT GAA TGC CGC CTG CTC GCC TAC ATA TCC CAG GTG 526
 Ala Glu Val Leu Ser Glu Cys Arg Leu Leu Ala Tyr Ile Ser Gln Val
 160 165 170 175
 CCC ACG CAG ATG TCC TTC CTC TTC CGC CTC ATC AAC ATC ATC CAC GTG 574
 Pro Thr Gln Met Ser Phe Leu Phe Arg Leu Ile Asn Ile Ile His Val
 180 185 190
 CAG ACG CTG ACC CAG GAG AAC GTC AGC TGC CTC AAC ACC AGC CTG GTG 622
 Gln Thr Leu Thr Gln Glu Asn Val Ser Cys Leu Asn Thr Ser Leu Val
 195 200 205
 ATC CTG ATG CTG GCC CGA CGG AAA GAG CGG CTG CCC CTG TAC CTG CGG 670
 Ile Leu Met Leu Ala Arg Arg Lys Glu Arg Leu Pro Leu Tyr Leu Arg
 210 215 220
 CTG CTG CAG CGG ATG GAG CAC AGC AAG AAG TAC CCC GGC TTC CTG CTC 718
 Leu Leu Gln Arg Met Glu His Ser Lys Lys Tyr Pro Gly Phe Leu Leu
 225 230 235
 AAC AAC TTC CAC AAC CTG CTG CGC TTC TGG CAG CAC TAC CTG CAC 766
 Asn Asn Phe His Asn Leu Leu Arg Phe Trp Gln Gln His Tyr Leu His
 240 245 250 255
 AAG GAC AAG GAC AGC ACC TGC CTA GAG AAC AGC TCC TGC ATC AGC TTC 814
 Lys Asp Lys Asp Ser Thr Cys Leu Glu Asn Ser Ser Cys Ile Ser Phe
 260 265 270
 TCA TAC TGG AAG GAG ACA GTG TCC ATC CTG TTG AAC CCG GAC CGG CAG 862
 Ser Tyr Trp Lys Glu Thr Val Ser Ile Leu Leu Asn Pro Asp Arg Gln
 275 280 285
 TCA CCC TCT CTC GTT AGC TAC ATT GAG GAG CCC TAC ATG GAC ATA 910
 Ser Pro Ser Ala Leu Val Ser Tyr Ile Glu Glu Pro Tyr Met Asp Ile
 290 295 300
 GAC AGG GAC TTC ACT GAG GAG TGACCTGGG CCAGGCCCTCG GGAGGCTGCT 961
 Asp Arg Asp Phe Thr Glu Glu
 305 310
 GGGCCAGTGT GGGTGAGCGT GGGTACGATG CCACACGCC TGCCCTGTC CCGTCCCTCC 1021
 CTGCTGCTCT CTGCCTGCC CAGGTCTTG GGTACAGGCT TGGTGGAGG GAAGTCCTAG 1081
 AAGCCCTTGG TCCCCCTGGG TCTGAGGGCC CTAGGTCATG GAGAGCCTCA GTCCCCATAA 1141
 TGAGGACAGG GTACCATGCC CACCTTCCT TCAGAACCTT GGGGCCAGG GCCACCCAGA 1201
 GGTAAGAGGA CATTAGCAT TAGCTCTGTG TGAGCTCCTG CCGGTTCTT GGCTGTCAGT 1261
 CAGTCCCAGA GTGGGGAGGA AGATATGGGT GACCCCCACC CCCCCATCTGT GAGCCAAGCC 1321
 TCCCTTGTCC CTGGCCTTG GACCCAGGCA AAGGCTCTG AGCCCTGGC AGGGGTGGTG 1381
 GGTACCAGAG AATGCTGCCT TCCCCCAAGC CTGCCCCCTCT GCCTCATTTT CCTGTAGCTC 1441
 CTCTGGTTCT GTTGCTCAT TGGCCGCTGT GTTCATCCAA GGGGGTTCTC CCAGAAGTGA 1501
 GGGGCCTTTC CCTCCATCCC TTGGGGCACG GGGCAGCTGT GCCTGCCCTG CCTCTGCCTG 1561

AGGCAGCCGC TCCTGCCTGA GCCTGGACAT GGGGCCCTTC CTTGTGTTGC CAATTTATTA	1621
ACAGCAAATA AACCAATTAA ATGGAGACTA TTAAATAACT TTATTTAAA AATGAAAAAA	1681
AAAAAAAAAA AAA	1694

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Leu Lys Ala Asn Ile Pro Glu Val Glu Ala Val Leu Asn Thr Asp	
1 5 10 15	
Arg Ser Leu Val Cys Asp Gly Lys Arg Gly Leu Leu Thr Arg Leu Leu	
20 25 30	
Gln Val Met Lys Lys Glu Pro Ala Glu Ser Ser Phe Arg Phe Trp Gln	
35 40 45	
Ala Arg Ala Val Glu Ser Phe Leu Arg Gly Thr Thr Ser Tyr Ala Asp	
50 55 60	
Gln Met Phe Leu Leu Lys Arg Gly Leu Leu Glu His Ile Leu Tyr Cys	
65 70 75 80	
Ile Val Asp Ser Glu Cys Lys Ser Arg Asp Val Leu Gln Ser Tyr Phe	
85 90 95	
Asp Leu Leu Gly Glu Leu Met Lys Phe Asn Val Asp Ala Phe Lys Arg	
100 105 110	
Phe Asn Lys Tyr Ile Asn Thr Asp Ala Lys Phe Gln Val Phe Leu Lys	
115 120 125	
Gln Ile Asn Ser Ser Leu Val Asp Ser Asn Met Leu Val Arg Cys Val	
130 135 140	
Thr Leu Ser Leu Asp Arg Phe Glu Asn Gln Val Asp Met Lys Val Ala	
145 150 155 160	
Glu Val Leu Ser Glu Cys Arg Leu Leu Ala Tyr Ile Ser Gln Val Pro	
165 170 175	
Thr Gln Met Ser Phe Leu Phe Arg Leu Ile Asn Ile Ile His Val Gln	
180 185 190	
Thr Leu Thr Gln Glu Asn Val Ser Cys Leu Asn Thr Ser Leu Val Ile	
195 200 205	
Leu Met Leu Ala Arg Arg Lys Glu Arg Leu Pro Leu Tyr Leu Arg Leu	
210 215 220	
Leu Gln Arg Met Glu His Ser Lys Lys Tyr Pro Gly Phe Leu Leu Asn	
225 230 235 240	
Asn Phe His Asn Leu Leu Arg Phe Trp Gln Gln His Tyr Leu His Lys	
245 250 255	
Asp Lys Asp Ser Thr Cys Leu Glu Asn Ser Ser Cys Ile Ser Phe Ser	

260

265

270

Tyr	Trp	Lys	Glu	Thr	Val	Ser	Ile	Leu	Leu	Asn	Pro	Asp	Arg	Gln	Ser
							275				280				285
Pro	Ser	Ala	Leu	Val	Ser	Tyr	Ile	Glu	Glu	Pro	Tyr	Met	Asp	Ile	Asp
						290		295				300			
Arg	Asp	Phe	Thr	Glu	Glu										
						305		310							

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: cDNA
- ii) HYPOTHETICAL: NO
- ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

G GAG ATC AGT CGG AAG GTG TAC AAG GGA ATG TTA GAC CTC CTC AAG Glu Ile Ser Arg Lys Val Tyr Lys Gly Met Leu Asp Leu Leu Lys 1 5 10 15	46
TGT ACA GTC CTC AGC TTG GAG CAG TCC TAT GCC CAC GCG GGT CTG GGT Cys Thr Val Leu Ser Leu Glu Gln Ser Tyr Ala His Ala Gly Leu Gly 20 25 30	94
GGC ATG GCC AGC ATC TTT GGG CTT TTG GAG ATT GCC CAG ACC CAC TAC Gly Met Ala Ser Ile Phe Gly Leu Leu Glu Ile Ala Gln Thr His Tyr 35 40 45	142
TAT AGT AAA GAA CCA GAC AAG CGG AAG AGA AGT CCA ACA GAA AGT GTA Tyr Ser Lys Glu Pro Asp Lys Arg Lys Arg Ser Pro Thr Glu Ser Val 50 55 60	190
AAT ACC CCA GTT GGC AAG GAT CCT GGC CTA GCT GGG CGG GGG GAC CCA Asn Thr Pro Val Gly Lys Asp Pro Gly Leu Ala Gly Arg Gly Asp Pro 65 70 75	238
AAG GCT ATG GCA CAA CTG AGA GTT CCA CAA CTG GGA CCT CGG GCA CCA Lys Ala Met Ala Gln Leu Arg Val Pro Gln Leu Gly Pro Arg Ala Pro 80 85 90 95	286
AGT GCC ACA GGA AAG GGT CCT AAG GAA CTG GAC ACC AGA AGT TTA AAG Ser Ala Thr Gly Lys Gly Pro Lys Glu Leu Asp Thr Arg Ser Leu Lys 100 105 110	334
GAA GAA AAT TTT ATA GCA TCT ATT GGG CCT GAA GTA ATC AAA CCT GTC Glu Glu Asn Phe Ile Ala Ser Ile Gly Pro Glu Val Ile Lys Pro Val 115 120 125	382
TTT GAC CTT GGT GAG ACA GAG GAG AAA AAG TCC CAG ATC AGC GCA GAC Phe Asp Leu Gly Glu Thr Glu Glu Lys Lys Ser Gln Ile Ser Ala Asp 130 135 140	430

AGT GGT GTG AGC CTG ACG TCT AGT TCC CAG AGG ACT GAT CAA GAC TCT Ser Gly Val Ser Leu Thr Ser Ser Ser Gln Arg Thr Asp Gln Asp Ser 145 150 155	478
GTC ATC GGC GTG AGT CCA GCT GTT ATG ATC CGC AGC TCA AGT CAG GAT Val Ile Gly Val Ser Pro Ala Val Met Ile Arg Ser Ser Ser Gln Asp 160 165 170 175	526
TCT GAA GTT AGC ACC GTG GTG AGT AAT AGC TCT GGA GAG ACC CTT GGA Ser Glu Val Ser Thr Val Val Ser Asn Ser Ser Gly Glu Thr Leu Gly 180 185 190	574
GCT GAC AGT GAC TTG AGC AGC AAT GCA GGT GAT GGA CCA GGT GGC GAG Ala Asp Ser Asp Leu Ser Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu 195 200 205	622
GGC AGT GTT CAC CTG GCA AGC TCT CGG GGC ACT TTG TCT GAT AGT GAA Gly Ser Val His Leu Ala Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu 210 215 220	670
ATT GAG ACC AAC TCT GCC ACA AGC ACC ATC TTT GGT AAA GCC CAC AGC Ile Glu Thr Asn Ser Ala Thr Ser Thr Ile Phe Gly Lys Ala His Ser 225 230 235	718
TTG AAG CCA AGC ATA AAG GAG AAG CTG GCA GGC AGC CCC ATT CGT ACT Leu Lys Pro Ser Ile Lys Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr 240 245 250 255	766
TCT GAA GAT GTG AGC CAG CGA GTC TAT CTC TAT GAG GGA CTC CTA GGC Ser Glu Asp Val Ser Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly 260 265 270	814
AAA GAG CGT TCT ACT TTA TGG GAC CAA ATG CAA TTC TGG GAA GAT GCC Lys Glu Arg Ser Thr Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala 275 280 285	862
TTC TTA GAT GCT GTG ATG TTG GAG AGA GAA GGG ATG GGT ATG GAC CAG Phe Leu Asp Ala Val Met Leu Glu Arg Glu Gly Met Gly Met Asp Gln 290 295 300	910
GGT CCC CAG GAA ATG ATC GAC AGG TAC CTG TCC CTT GGA GAA CAT GAC Gly Pro Gln Glu Met Ile Asp Arg Tyr Leu Ser Leu Gly Glu His Asp 305 310 315	958
CGG AAG CGC CTG GAA GAT GAT GAA GAT CGC TTG CTG GCC ACA CTT CTG Arg Lys Arg Leu Glu Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu 320 325 330 335	1006
CAC AAC CTC ATC TCC TAC ATG CTG CTG ATG AAG GTA AAT AAG AAT GAC His Asn Leu Ile Ser Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp 340 345 350	1054
ATC CGC AAG AAG GTG AGG CGC CTA ATG GGA AAG TCG CAC ATT GGG CTT Ile Arg Lys Lys Val Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu 355 360 365	1102
GTG TAC AGC CAG CAA ATC AAT GAG GTG CTT GAT CAG CTG GCG AAC CTG Val Tyr Ser Gln Gln Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu 370 375 380	1150
AAT GGA CGC GAT CTC TCT ATC TGG TCC AGT GGC AGC CGG CAC ATG AAG Asn Gly Arg Asp Leu Ser Ile Trp Ser Ser Gly Ser Arg His Met Lys 385 390 395	1193
AAG CAG ACA TTT GTG GTA CAT GCA GGG ACA GAT ACA AAC GGA GAT ATC Lys Gln Thr Phe Val Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile 400 405 410 415	1246

TTT TTC ATG GAG GTG TGC GAT GAC TGT GTG GTG TTG CGT AGT AAC ATC Phe Phe Met Glu Val Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile 420 425 430	1294
GGA ACA GTG TAT GAG CGC TGG TGG TAC GAG AAG CTC ATC AAC ATG ACC Gly Thr Val Tyr Glu Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr 435 440 445	1342
TAC TGT CCC AAG ACG AAG GTG TTG TGC TTG TGG CGT AGA AAT GGC TCT Tyr Cys Pro Lys Thr Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser 450 455 460	1390
GAG ACC CAG CTC AAC AAG TTC TAT ACT AAA AAG TGT CGG GAG CTG TAC Glu Thr Gln Leu Asn Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr 465 470 475	1438
TAC TGT GTG AAG GAC AGC ATG GAG CGC GCT GCC GCC CGA CAG CAA AGC Tyr Cys Val Lys Asp Ser Met Glu Arg Ala Ala Ala Arg Gln Gln Ser 480 485 490 495	1486
ATC AAA CCC GGA CCT GAA TTG GGT GGC GAG TTC CCT GTG CAG GAC CTG Ile Lys Pro Gly Pro Glu Leu Gly Glu Phe Pro Val Gln Asp Leu 500 505 510	1534
AAG ACT GGT GAG GGT GGC CTG CTG CAG GTG ACC CTG GAA GGG ATC AAC Lys Thr Gly Glu Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn 515 520 525	1582
CTC AAA TTC ATG CAC AAT CAG GTT TTC ATA GAG CTG AAT CAC ATT AAA Leu Lys Phe Met His Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys 530 535 540	1630
AAG TGC AAT ACA GTT CGA GGC GTC TTT GTC CTG GAG GAA TTT GTT CCT Lys Cys Asn Thr Val Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro 545 550 555	1678
GAA ATT AAA GAA GTG GTG AGC CAC AAG TAC AAG ACA CCA ATG GCC CAC Glu Ile Lys Glu Val Val Ser His Lys Tyr Lys Thr Pro Met Ala His 560 565 570 575	1726
GAA ATC TGC TAC TCC GTA TTA TGT CTC TTC TCG TAC GTG GCT GCA GTT Glu Ile Cys Tyr Ser Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val 580 585 590	1774
CAT AGC AGT GAG GAA GAT CTC AGA ACC CCG CCC CGG CCT GTC TCT AGC His Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser 595 600 605	1822
TGATGGAGAG GGGCTACGCA GCTGCCCGAG CCCAGGGCAC GCCCTGGCC CCTTGCTGTT	1882
CCCAAGTGCA CGATGCTGCT GTGACTGAGG AGTGGATGAT GCTCGTGTGT CCTCTGCAAG	1942
CCCCCTGCTG TGGCTTGGTT GTTACCGGT TATGTGTCCC TCTGAGTGTG TCTTGAGCGT	2002
GTCCACCTTC TCCCTCTCCA CTCCCAGAAG ACCAAACTGC CTTCCCTCA GGGCTCAAGA	2062
ATGTGTACAG TCTGTGGGGC CGGTGTGAAC CCACTATTTT GTGTCCTTGA GACATTGTG	2122
TTGTGGTTCC TTGTCCTTGT CCCTGGCGTT ATAACGTGCC ACTGCAAGAG TCTGGCTCTC	2182
CCTTCTCTGT GACCCGGCAT GACTGGCGC CTGGAGCAGT TTCACCTCTGT GAGGAGTGTG	2242
GGAACCTGG GGCTCACCCCT CTCAGAGGAA GGGCACAGAG AGGAAGGGAA GAATTGGGGG	2302
GCAGCCGGAG TGAGTGGCAG CCTCCCTGCT TCCTTCTGCA TTCCCAAGCC GGCAGCTACT	2362
GCCCCAGGGCC CGCAGTGTG TGCTGCTGCC GCCACAGCCT CTGTGACTGC AGTGGAGCGG	2422

CGAATTCCCT GTGGCCTGCC ACGCCTTCGG CATCAGAGGA TGGAGTGGTC GAGGCTAGTG	2482
GAGTCCCAGG GACCGCTGGC TGCTCTGCCT GAGCATCAGG GAGGGGGCAG GAAAGACCAA	2542
GCTGGGTTTG CACATCTGTC TGCAGGCTGT CTCTCCAGGC ACGGGGTGTC AGGAGGGAGA	2602
GACAGCCTGG GTATGGCAA GAAATGACTG TAAATATTTC AGCCCCACAT TATTTATAGA	2662
AAATGTACAG TTGTGTGAAT GTGAAATAAA TGTCCCTAAC TCCCCAAAAAA AAAAAAAA	2722
AAAAAAA AAA	2735

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 607 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Ile Ser Arg Lys Val Tyr Lys Gly Met Leu Asp Leu Leu Lys Cys	
1 5 10 15	
Thr Val Leu Ser Leu Glu Gln Ser Tyr Ala His Ala Gly Leu Gly Gly	
20 25 30	
Met Ala Ser Ile Phe Gly Leu Leu Glu Ile Ala Gln Thr His Tyr Tyr	
35 40 45	
Ser Lys Glu Pro Asp Lys Arg Lys Arg Ser Pro Thr Glu Ser Val Asn	
50 55 60	
Thr Pro Val Gly Lys Asp Pro Gly Leu Ala Gly Arg Gly Asp Pro Lys	
65 70 75 80	
Ala Met Ala Gln Leu Arg Val Pro Gln Leu Gly Pro Arg Ala Pro Ser	
85 90 95	
Ala Thr Gly Lys Gly Pro Lys Glu Leu Asp Thr Arg Ser Leu Lys Glu	
100 105 110	
Glu Asn Phe Ile Ala Ser Ile Gly Pro Glu Val Ile Lys Pro Val Phe	
115 120 125	
Asp Leu Gly Glu Thr Glu Glu Lys Ser Gln Ile Ser Ala Asp Ser	
130 135 140	
Gly Val Ser Leu Thr Ser Ser Ser Gln Arg Thr Asp Gln Asp Ser Val	
145 150 155 160	
Ile Gly Val Ser Pro Ala Val Met Ile Arg Ser Ser Ser Gln Asp Ser	
165 170 175	
Glu Val Ser Thr Val Val Ser Asn Ser Ser Gly Glu Thr Leu Gly Ala	
180 185 190	
Asp Ser Asp Leu Ser Ser Asn Ala Gly Asp Gly Pro Gly Glu Gly	
195 200 205	
Ser Val His Leu Ala Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile	
210 215 220	
Glu Thr Asn Ser Ala Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu	

225	230	235	240
Lys Pro Ser Ile Lys Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser			
245	250	255	
Glu Asp Val Ser Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys			
260	265	270	
Glu Arg Ser Thr Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe			
275	280	285	
Leu Asp Ala Val Met Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly			
290	295	300	
Pro Gln Glu Met Ile Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg			
305	310	315	320
Lys Arg Leu Glu Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His			
325	330	335	
Asn Leu Ile Ser Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile			
340	345	350	
Arg Lys Lys Val Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu Val			
355	360	365	
Tyr Ser Gln Gln Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn			
370	375	380	
Gly Arg Asp Leu Ser Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys			
385	390	395	400
Gln Thr Phe Val Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe			
405	410	415	
Phe Met Glu Val Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly			
420	425	430	
Thr Val Tyr Glu Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr			
435	440	445	
Cys Pro Lys Thr Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu			
450	455	460	
Thr Gln Leu Asn Lys Phe Tyr Thr Lys Cys Arg Glu Leu Tyr Tyr			
465	470	475	480
Cys Val Lys Asp Ser Met Glu Arg Ala Ala Arg Gln Gln Ser Ile			
485	490	495	..
Lys Pro Gly Pro Glu Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys			
500	505	510	
Thr Gly Glu Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu			
515	520	525	
Lys Phe Met His Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys			
530	535	540	
Cys Asn Thr Val Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu			
545	550	555	560
Ile Lys Glu Val Val Ser His Lys Tyr Lys Thr Pro Met Ala His Glu			
565	570	575	
Ile Cys Tyr Ser Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His			
580	585	590	

Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser
 595 600 605

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..2846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CC CAG ACT CGC CCC GCC CCA GAG ACT GCG CCT CCG CGG GCA CGA GAC Gln Thr Arg Pro Ala Pro Glu Thr Ala Pro Ala Arg Ala Arg Asp	47
1 5 10 15	
ACC CTC TCC GCG ATG ACT GCC AGC TCA GTG GAG CAG CTG CGG AAG GAG Thr Leu Ser Ala Met Thr Ala Ser Ser Val Glu Gln Leu Arg Lys Glu	95
20 25 30	
GGC AAT GAG CTG TTC AAA TGT GGA GAC TAC GGG GGC GCC CTG GCG GCC Gly Asn Glu Leu Phe Lys Cys Gly Asp Tyr Gly Gly Ala Leu Ala Ala	143
35 40 45	
TAC ACT CAG GCC CTG GGT CTG GAC GCG ACG CCC CAG GAC CAG GCC GTT Tyr Thr Gln Ala Leu Gly Leu Asp Ala Thr Pro Gln Asp Gln Ala Val	191
50 55 60	
CTG CAC CGG AAC CGG GCC TGC CAC CTC AAG CTG GAA GAT TAC GAC Leu His Arg Asn Arg Ala Ala Cys His Leu Lys Leu Glu Asp Tyr Asp	239
65 70 75	
AAA GCA GAA ACA GAG GCA TCC AAA GCC ATT GAA AAG GAT GGT GGG GAT Lys Ala Glu Thr Glu Ala Ser Lys Ala Ile Glu Lys Asp Gly Gly Asp	287
80 85 90 95	
GTC AAA GCA CTC TAC CGG CGG AGC CAA GCC CTA GAG AAG CTG GGC CGC Val Lys Ala Leu Tyr Arg Arg Ser Gln Ala Leu Glu Lys Leu Gly Arg	335
100 105 110	
CTG GAC CAG GCT GTC CTT GAC CTG CAG AGA TGT GTG AGC TTG GAG CCC Leu Asp Gln Ala Val Leu Asp Leu Gln Arg Cys Val Ser Leu Glu Pro	383
115 120 125	
AAG AAC AAA GTT TTC CAG GAG GCC TTG CGG AAC ATC GGG GGC CAG ATT Lys Asn Lys Val Phe Gln Glu Ala Leu Arg Asn Ile Gly Gly Gln Ile	431
130 135 140	
CAG GAG AAG GTG CGA TAC ATG TCC TCG ACG GAT GCC AAA GTG GAA CAG Gln Glu Lys Val Arg Tyr Met Ser Ser Thr Asp Ala Lys Val Glu Gln	479
145 150 155	

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ATG TTT CAG ATA CTG TTG GAC CCA GAA GAG AAG GGC ACT GAG AAA AAG Met Phe Gln Ile Leu Leu Asp Pro Glu Glu Lys Gly Thr Glu Lys Lys 160 165 170 175	527
CAA AAG GCT TCT CAG AAC CTG GTG CTG GCC AGG GAG GAT GCT GGA Gln Lys Ala Ser Gln Asn Leu Val Val Ala Arg Glu Asp Ala Gly 180 185 190	575
GCG GAG AAG ATC TTC CCG AGT AAT GGG GTT CAG CTC TTG CAA CGT TTA Ala Glu Lys Ile Phe Arg Ser Asn Gly Val Gln Leu Leu Gln Arg Leu 195 200 205	623
CTG GAC ATG GGA GAG ACT GAC CTC ATG CTG GCG GCT CTG CGT ACG CTG Leu Asp Met Gly Glu Thr Asp Leu Met Leu Ala Ala Leu Arg Thr Leu 210 215 220	671
GTT GGC ATT TGC TCT GAG CAT CAG TCA CGG ACA GTG GCA ACC CTG AGC Val Gly Ile Cys Ser Glu His Gln Ser Arg Thr Val Ala Thr Leu Ser 225 230 235	719
ATA CTG GGA ACT CGG CGA GTA GTC TCC ATC CTG GGC GTG GAA AGC CAG Ile Leu Gly Thr Arg Arg Val Val Ser Ile Leu Gly Val Glu Ser Gln 240 245 250 255	767
GCT GTG TCC CTG GCT GCC TGC CAC CTG CTG CAG GTT ATG TTT GAT GCC Ala Val Ser Leu Ala Ala Cys His Leu Leu Gln Val Met Phe Asp Ala 260 265 270	815
CTC AAG GAA GGT GTC AAA AAA GGC TTC CGA GGC AAA GAA GGT GCC ATC Leu Lys Glu Gly Val Lys Gly Phe Arg Gly Lys Glu Gly Ala Ile 275 280 285	863
ATT GTG GAT CCT GCC CGG GAG CTG AAG GTC CTC ATC AGT AAC CTC TTA Ile Val Asp Pro Ala Arg Glu Leu Lys Val Leu Ile Ser Asn Leu Leu 290 295 300	911
GAT CTG CTG ACA GAG GTG GGG GTC TCT GGC CAA GGC CGA GAC AAT GCC Asp Leu Leu Thr Glu Val Gly Val Ser Gly Gln Gly Arg Asp Asn Ala 305 310 315	959
CTG ACC CTC CTG ATT AAA GCG GTG CCC CGG AAG TCT CTC AAG GAC CCC Leu Thr Leu Leu Ile Lys Ala Val Pro Arg Lys Ser Leu Lys Asp Pro 320 325 330 335	1007
AAC AAC AGC CTC ACC CTC TGG GTC ATC GAC CAA GGT CTG AAA AAG ATT Asn Asn Ser Leu Thr Leu Trp Val Ile Asp Gln Gly Leu Lys Lys Ile 340 345 350	1055
TTG GAA GTG GGG GGC TCT CTA CAG GAC CCT CCT GGG GAG CTC GCA GTG Leu Glu Val Gly Gly Ser Leu Gln Asp Pro Pro Gly Glu Leu Ala Val 355 360 365	1103
ACC GCA AAC AGC CGC ATG AGC GCC TCT ATT CTC CTC AGC AAG CTC TTT Thr Ala Asn Ser Arg Met Ser Ala Ser Ile Leu Leu Ser Lys Leu Phe 370 375 380	1151
GAT GAC CTC AAG TGT GAT GCG GAG AGG GAG AAT TTC CAC AGA CTT TGT Asp Asp Leu Lys Cys Asp Ala Glu Arg Glu Asn Phe His Arg Leu Cys 385 390 395	1199
GAA AAC TAC ATC AAG AGC TGG TTT GAG GGC CAA GGG CTG GCC GGG AAG Glu Asn Tyr Ile Lys Ser Trp Phe Glu Gly Gln Gly Leu Ala Gly Lys 400 405 410 415	1247
CTA CGG GCC ATC CAG ACG GTG TCC TGC CTC CTG CAG GCC CCA TGT GAC Leu Arg Ala Ile Gln Thr Val Ser Cys Leu Leu Gln Gly Pro Cys Asp 420 425 430	1295

GCT GGC AAC CGG GCC TTG GAG CTG AGC GGT GTC ATG GAG AGT GTG ATT Ala Gly Asn Arg Ala Leu Glu Leu Ser Gly Val Met Glu Ser Val Ile 435 440 445	1343
GCT CTG TGT GCC TCT GAG CAG GAG GAG CAG CTG GTG GCC CTG GAG Ala Leu Cys Ala Ser Glu Gln Glu Glu Glu Gln Leu Val Ala Val Glu 450 455 460	1391
GCT CTG ATC CAT GCA GCC GGC AAG GCT AAG CGG GCC TCA TTC ATC ACT Ala Leu Ile His Ala Ala Gly Lys Ala Lys Arg Ala Ser Phe Ile Thr 465 470 475	1439
GCC AAT GGT GTC TCG CTG CTG AAG GAC CTA TAT AAG TGC AGC GAG AAG Ala Asn Gly Val Ser Leu Leu Lys Asp Leu Tyr Lys Cys Ser Glu Lys 480 485 490 495	1487
GAC AGC ATC CGC ATC CGG GCG CTA GTG GGA CTC TGT AAG CTC GGT TCG Asp Ser Ile Arg Ile Arg Ala Leu Val Gly Leu Cys Lys Leu Gly Ser 500 505 510	1535
GCT GGA GGG ACT GAC TTC AGC ATG AAG CAG TTT GCT GAA GGC TCC ACT Ala Gly Gly Thr Asp Phe Ser Met Lys Gln Phe Ala Glu Gly Ser Thr 515 520 525	1583
CTC AAA CTG GCT AAG CAG TGT CGA AAG TGG CTG TGC AAT GAC CAG ATC Leu Lys Leu Ala Lys Gln Cys Arg Lys Trp Leu Cys Asn Asp Gln Ile 530 535 540	1631
GAC GCA GGC ACT CGG CGC TGG GCA GTG GAG GGC CTG GCT TAC CTG ACC Asp Ala Gly Thr Arg Arg Trp Ala Val Glu Gly Leu Ala Tyr Leu Thr 545 550 555	1679
TTT GAT GCC GAC GTG AAG GAA GAG TTT GTG GAG GAT GCG GCT GCT CTG Phe Asp Ala Asp Val Lys Glu Glu Phe Val Glu Asp Ala Ala Ala Leu 560 565 570 575	1727
AAA GCT CTG TTC CAG CTC AGC AGG TTG GAG GAG AGG TCA GTG CTC TTT Lys Ala Leu Phe Gln Leu Ser Arg Leu Glu Glu Arg Ser Val Leu Phe 580 585 590	1775
GCG GTG GCC TCA GCG CTG GTG AAC TGC ACC AAC AGC TAT GAC TAC GAG Ala Val Ala Ser Ala Leu Val Asn Cys Thr Asn Ser Tyr Asp Tyr Glu 595 600 605	1823
GAG CCC GAC CCC AAG ATG GTG GAG CTG GCC AAG TAT GCC AAG CAG CAT Glu Pro Asp Pro Lys Met Val Glu Leu Ala Lys Tyr Ala Lys Gln His 610 615 620	1871
GTG CCC GAG CAG CAC CCC AAG GAC AAG CCA AGC TTC GTG CGG GCT CGG Val Pro Glu Gln His Pro Lys Asp Lys Pro Ser Phe Val Arg Ala Arg 625 630 635	1919
GTG AAG AAG CTG CTG GCA GCG GGT GTG GTG TCG GCC ATG GTG TGC ATG Val Lys Lys Leu Leu Ala Ala Gly Val Val Ser Ala Met Val Cys Met 640 645 650 655	1967
GTG AAG ACG GAG AGC CCT GTG CTG ACC AGT TCC TGC AGA GAG CTG CTC Val Lys Thr Glu Ser Pro Val Leu Thr Ser Ser Cys Arg Glu Leu Leu 660 665 670	2015
TCC AGG GTC TTC TTG GCT TTA GTG GAA GAG GTA GAG GAC CGA GGC ACT Ser Arg Val Phe Leu Ala Leu Val Glu Glu Val Glu Asp Arg Gly Thr 675 680 685	2063
GTG GTT GCC CAG GGA GGC GGC AGG GCG CTG ATC CCG CTG GCC CTG GAA Val Val Ala Gln Gly Gly Arg Ala Leu Ile Pro Leu Ala Leu Glu 690 695 700	2111

GGC ACG GAC GTG GGG CAG ACA AAG GCA GCC CAG GCC CTT GCC AAG CTC Gly Thr Asp Val Gly Gln Thr Lys Ala Ala Gln Ala Leu Ala Lys Leu 705 710 715	2159
ACC ATC ACC TCC AAC CCG GAG ATG ACC TTC CCT GGC GAG CGG ATC TAT Thr Ile Thr Ser Asn Pro Glu Met Thr Phe Pro Gly Glu Arg Ile Tyr 720 725 730 735	2207
GAG GTG GTC CGG CCC CTC GTC TCC CTG TTG CAC CTC AAC TGC TCA GGC Glu Val Val Arg Pro Leu Val Ser Leu Leu His Leu Asn Cys Ser Gly 740 745 750	2255
CTG CAG AAC TTC GAG GCG CTC ATG GCC CTA ACA AAC CTG GCT GGG ATC Leu Gln Asn Phe Glu Ala Leu Met Ala Leu Thr Asn Leu Ala Gly Ile 755 760 765	2303
AGC GAG AGG CTC CGG CAG AAG ATC CTG AAG GAG AAG GCT GTG CCC ATG Ser Glu Arg Leu Arg Gln Lys Ile Leu Lys Glu Lys Ala Val Pro Met 770 775 780	2351
ATA GAA GGC TAC ATG TTT GAG GAG CAT GAG ATG ATC CGC CGG GCA GCC Ile Glu Gly Tyr Met Phe Glu Glu His Glu Met Ile Arg Arg Ala Ala 785 790 795	2399
ACG GAG TGC ATG TGT AAC TTG GCC ATG AGC AAG GAG GTG CAG GAC CTC Thr Glu Cys Met Cys Asn Leu Ala Met Ser Lys Glu Val Gln Asp Leu 800 805 810 815	2447
TTC GAA GCC CAG GGC AAT GAC CGA CTG AAG CTG CTG GTG CTG TAC AGT Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys Leu Leu Val Leu Tyr Ser 820 825 830	2495
GGA GAG GAT GAT GAG CTG CTA CAG CGG GCA GCT GCC GGG GGC TTG GCC Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala Ala Gly Gly Leu Ala 835 840 845	2543
ATG CTT ACC TCC ATG CGG CCC ACG CTC TGC AGC CGC ATT CCC CAA GTG Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser Arg Ile Pro Gln Val 850 855 860	2591
ACC ACA CAC TGG CTG GAG ATC CTG CAG GCC CTG CTT CTG AGC TCC AAC Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu Leu Ser Ser Asn 865 870 875	2639
CAG GAG CTG CAG CAC CGG GGT GCT GTG GTG CTG AAC ATG GTG GAG Gln Glu Leu Gln His Arg Gly Ala Val Val Val Leu Asn Met Val Glu 880 885 890 895	2687
GCC TCG AGG GAG ATT GCC AGC ACC CTG ATG GAG AGT GAG ATG ATG GAG Ala Ser Arg Glu Ile Ala Ser Thr Leu Met Glu Ser Glu Met Met Glu 900 905 910	2735
ATC TTG TCA GTG CTA GCT AAG GGT GAC CAC AGC CCT GTC ACA AGG GCT Ile Leu Ser Val Leu Ala Lys Gly Asp His Ser Pro Val Thr Arg Ala 915 920 925	2783
GCT GCA GCC TGC CTG GAC AAA GCA GTG GAA TAT GGG CTT ATC CAA CCC Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr Gly Leu Ile Gln Pro 930 935 940	2831
AAC CAA GAT GGA GAG TGAGGGGTT GTCCCTGGC CCAAGGCTCA TGCACACGCT Asn Gln Asp Gly Glu 945	2886
ACCTATTGTG GCACGGAGAG TAAGGACGGA AGCAGCTTTG GCTGGTGGTG GCTGGCATGC	2946
CCAATACTCT TGCCCATCCT CGCTTGCTGC CCTAGGATGT CCTCTGTTCT GAGTCAGCGG	3006

CCACGTTAG TCACACAGCC CTGCTTGGCC AGCACTGCCT GCAGCCTCAC TCAGAGGGC	3066
CCTTTTCTG TACTACTGTA GTCAGCTGGG AATGGGGAAG GTGCATCCCA ACACAGCCTG	3126
TGGATCCTGG GGCATTTGGA AGGGCGCACA CATCAGCAGC CTCACCAGCT GTGAGCCTGC	3186
TATCAGGCCCT GCCCCTCCAA TAAAAGTGTG TAGAACTCC	3225

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Thr Arg Pro Ala Pro Glu Thr Ala Pro Ala Arg Ala Arg Asp Thr	
1 5 . 10 15	
Leu Ser Ala Met Thr Ala Ser Ser Val Glu Gln Leu Arg Lys Glu Gly	
20 25 30	
Asn Glu Leu Phe Lys Cys Gly Asp Tyr Gly Gly Ala Leu Ala Ala Tyr	
35 40 45	
Thr Gln Ala Leu Gly Leu Asp Ala Thr Pro Gln Asp Gln Ala Val Leu	
50 55 60	
His Arg Asn Arg Ala Ala Cys His Leu Lys Leu Glu Asp Tyr Asp Lys	
65 70 75 80	
Ala Glu Thr Glu Ala Ser Lys Ala Ile Glu Lys Asp Gly Gly Asp Val	
85 90 95	
Lys Ala Leu Tyr Arg Arg Ser Gln Ala Leu Glu Lys Leu Gly Arg Leu	
100 105 110	
Asp Gln Ala Val Leu Asp Leu Gln Arg Cys Val Ser Leu Glu Pro Lys	
115 120 125	
Asn Lys Val Phe Gln Glu Ala Leu Arg Asn Ile Gly Gly Gln Ile Gln	
130 135 140	
Glu Lys Val Arg Tyr Met Ser Ser Thr Asp Ala Lys Val Glu Gln Met	
145 150 155 160 ..	
Phe Gln Ile Leu Leu Asp Pro Glu Glu Lys Gly Thr Glu Lys Lys Gln	
165 170 175	
Lys Ala Ser Gln Asn Leu Val Val Leu Ala Arg Glu Asp Ala Gly Ala	
180 185 190	
Glu Lys Ile Phe Arg Ser Asn Gly Val Gln Leu Leu Gln Arg Leu Leu	
195 200 205	
Asp Met Gly Glu Thr Asp Leu Met Leu Ala Ala Leu Arg Thr Leu Val	
210 215 220	
Gly Ile Cys Ser Glu His Gln Ser Arg Thr Val Ala Thr Leu Ser Ile	
225 230 235 240	
Leu Gly Thr Arg Arg Val Val Ser Ile Leu Gly Val Glu Ser Gln Ala	
245 250 255	

Val Ser Leu Ala Ala Cys His Leu Leu Gln Val Met Phe Asp Ala Leu
260 265 270
Lys Glu Gly Val Lys Lys Gly Phe Arg Gly Lys Glu Gly Ala Ile Ile
275 280 285
Val Asp Pro Ala Arg Glu Leu Lys Val Leu Ile Ser Asn Leu Leu Asp
290 295 300
Leu Leu Thr Glu Val Gly Val Ser Gly Gln Gly Arg Asp Asn Ala Leu
305 310 315 320
Thr Leu Leu Ile Lys Ala Val Pro Arg Lys Ser Leu Lys Asp Pro Asn
325 330 335
Asn Ser Leu Thr Leu Trp Val Ile Asp Gln Gly Leu Lys Ile Leu
340 345 350
Glu Val Gly Gly Ser Leu Gln Asp Pro Pro Gly Glu Leu Ala Val Thr
355 360 365
Ala Asn Ser Arg Met Ser Ala Ser Ile Leu Leu Ser Lys Leu Phe Asp
370 375 380
Asp Leu Lys Cys Asp Ala Glu Arg Glu Asn Phe His Arg Leu Cys Glu
385 390 395 400
Asn Tyr Ile Lys Ser Trp Phe Glu Gly Gln Gly Leu Ala Gly Lys Leu
405 410 415
Arg Ala Ile Gln Thr Val Ser Cys Leu Leu Gln Gly Pro Cys Asp Ala
420 425 430
Gly Asn Arg Ala Leu Glu Leu Ser Gly Val Met Glu Ser Val Ile Ala
435 440 445
Leu Cys Ala Ser Glu Gln Glu Glu Glu Gln Leu Val Ala Val Glu Ala
450 455 460
Leu Ile His Ala Ala Gly Lys Ala Lys Arg Ala Ser Phe Ile Thr Ala
465 470 475 480
Asn Gly Val Ser Leu Leu Lys Asp Leu Tyr Lys Cys Ser Glu Lys Asp
485 490 495
Ser Ile Arg Ile Arg Ala Leu Val Gly Leu Cys Lys Leu Gly Ser Ala
500 505 510
Gly Gly Thr Asp Phe Ser Met Lys Gln Phe Ala Glu Gly Ser Thr Leu
515 520 525
Lys Leu Ala Lys Gln Cys Arg Lys Trp Leu Cys Asn Asp Gln Ile Asp
530 535 540
Ala Gly Thr Arg Arg Trp Ala Val Glu Gly Leu Ala Tyr Leu Thr Phe
545 550 555 560
Asp Ala Asp Val Lys Glu Glu Phe Val Glu Asp Ala Ala Leu Lys
565 570 575
Ala Leu Phe Gln Leu Ser Arg Leu Glu Glu Arg Ser Val Leu Phe Ala
580 585 590
Val Ala Ser Ala Leu Val Asn Cys Thr Asn Ser Tyr Asp Tyr Glu Glu
595 600 605
Pro Asp Pro Lys Met Val Glu Leu Ala Lys Tyr Ala Lys Gln His Val

6293360 413003

610

615

620

Pro Glu Gln His Pro Lys Asp Lys Pro Ser Phe Val Arg Ala Arg Val
625 630 635 640

Lys Lys Leu Leu Ala Ala Gly Val Val Ser Ala Met Val Cys Met Val
645 650 655

Lys Thr Glu Ser Pro Val Leu Thr Ser Ser Cys Arg Glu Leu Leu Ser
660 665 670

Arg Val Phe Leu Ala Leu Val Glu Glu Val Glu Asp Arg Gly Thr Val
675 680 685

Val Ala Gln Gly Gly Gly Arg Ala Leu Ile Pro Leu Ala Leu Glu Gly
690 695 700

Thr Asp Val Gly Gln Thr Lys Ala Ala Gln Ala Leu Ala Lys Leu Thr
705 710 715 720

Ile Thr Ser Asn Pro Glu Met Thr Phe Pro Gly Glu Arg Ile Tyr Glu
725 730 735

Val Val Arg Pro Leu Val Ser Leu Leu His Leu Asn Cys Ser Gly Leu
740 745 750

Gln Asn Phe Glu Ala Leu Met Ala Leu Thr Asn Leu Ala Gly Ile Ser
755 760 765

Glu Arg Leu Arg Gln Lys Ile Leu Lys Glu Lys Ala Val Pro Met Ile
770 775 780

Glu Gly Tyr Met Phe Glu Glu His Glu Met Ile Arg Arg Ala Ala Thr
785 790 795 800

Glu Cys Met Cys Asn Leu Ala Met Ser Lys Glu Val Gln Asp Leu Phe
805 810 815

Glu Ala Gln Gly Asn Asp Arg Leu Lys Leu Leu Val Leu Tyr Ser Gly
820 825 830

Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala Gly Gly Leu Ala Met
835 840 845

Leu Thr Ser Met Arg Pro Thr Leu Cys Ser Arg Ile Pro Gln Val Thr
850 855 860

Thr His Trp Leu Glu Ile Leu Gln Ala Leu Leu Leu Ser Ser Asn Gln
865 870 875 880

Glu Leu Gln His Arg Gly Ala Val Val Val Leu Asn Met Val Glu Ala
885 890 895

Ser Arg Glu Ile Ala Ser Thr Leu Met Glu Ser Glu Met Met Glu Ile
900 905 910

Leu Ser Val Leu Ala Lys Gly Asp His Ser Pro Val Thr Arg Ala Ala
915 920 925

Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr Gly Leu Ile Gln Pro Asn
930 935 940

Gln Asp Gly Glu
945

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6002 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 326..5092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACGTGCATG	TGTAGCATGC	CTTGGTTTTT	CCTTTGGCAT	CTGAAAAAGG	CACAACCTGA	60
AAGACCTAGA	ACCCAGTGTG	GGTCCCCAGG	CCCTTTGGGA	CAGGAAGAGA	AGAGCCGTGT	120
GGCCGGGGGG	AGGATGTCT	GCGCGGGGGC	TGTCTCGCG	GACTGACTGG	ACTCCATCTC	180
CCAGCGGGCG	CCGCAGCGCG	GCCACGCC	CCCACCCCC	GCGCGGCC	GGTGGAGACT	240
TCGATTTCA	GAATTCTCC	TGGGAATGCT	GACTCCTTGC	TTGGTGCCT	GATGCTTCTC	300
TCAGATAAAC	TGATGAATTG	GAACC	ATG GTG CAA AAG AAG	AAG TTC TGT CCT	Met Val Gln Lys Lys Lys Phe Cys Pro	352
			1	5		
CGG TTA CTT GAC TAT CTA GTG ATC GTA GGG	GCC AGG CAC CCG	AGC AGT	400			
Arg Leu Leu Asp Tyr Leu Val Ile Val Gly Ala Arg His Pro Ser Ser	10 15 20	25				
GAT AGC GTG GCC CAG ACT CCT GAA TTG CTA CGG CGA TAC CCC TTG GAG	448					
Asp Ser Val Ala Gln Thr Pro Glu Leu Leu Arg Arg Tyr Pro Leu Glu	30 35 40					
GAT CAC ACT GAG TTT CCC CTG CCC CCA GAT GTA GTG TTC TTC TGC CAG	496					
Asp His Thr Glu Phe Pro Leu Pro Pro Asp Val Val Phe Phe Cys Gin	45 50 55					
CCC GAG GGC TGC CTG AGC GTG CGG CAG CGG CGC ATG AGC CTT CGG GAT	544					
Pro Glu Gly Cys Leu Ser Val Arg Gln Arg Arg Met Ser Leu Arg Asp	60 65 70					
GAT ACC TCT TTT GTC TTC ACC CTC ACT GAC AAG GAC ACT GGA GTC ACG	592					
Asp Thr Ser Phe Val Phe Thr Leu Thr Asp Lys Asp Thr Gly Val Thr	75 80 85					
CGA TAT GGC ATC TGT GTT AAC TTC TAC CGC TCC TTC CAA AAG CGA ATC	640					
Arg Tyr Gly Ile Cys Val Asn Phe Tyr Arg Ser Phe Gln Lys Arg Ile	90 95 100	105				
TCT AAG GAG AAG GGG GAA GGT GGG GCA GGG TCC CGT GGG AAG GAA GGA	688					
Ser Lys Glu Lys Gly Glu Gly Ala Gly Ser Arg Gly Lys Glu Gly	110 115 120					
ACC CAT GCC ACC TGT GCC TCA GAA GAG GGT GGC ACT GAG AGC TCA GAG	736					
Thr His Ala Thr Cys Ala Ser Glu Glu Gly Gly Thr Glu Ser Ser Glu	125 130 135					
AGT GGC TCA TCC CTG CAG CCT CTC AGT GCT GAC TCT ACC CCT GAT GTG	784					
Ser Gly Ser Ser Leu Gln Pro Leu Ser Ala Asp Ser Thr Pro Asp Val	140 145 150					

Sequence Data

AAC CAG TCT CCT CGG GGC AAA CGC CGG GCC AAG GCG GGG AGC CGC TCC Asn Gln Ser Pro Arg Gly Lys Arg Arg Ala Lys Ala Gly Ser Arg Ser 155 160 165	832
CGC AAC AGT ACT CTC ACG TCC CTG TGC GTG CTC AGC CAC TAC CCT TTC Arg Asn Ser Thr Leu Thr Ser Leu Cys Val Leu Ser His Tyr Pro Phe 170 175 180 185	880
TTC TCC ACC TTC CGA GAG TGT TTG TAT ACT CTC AAG CGC CTG GTG GAC Phe Ser Thr Phe Arg Glu Cys Leu Tyr Thr Leu Lys Arg Leu Val Asp 190 195 200	928
TGC TGT AGT GAG CGC CTT CTG GGC AAG AAA CTG GGC ATC CCT CGA GGC Cys Cys Ser Glu Arg Leu Leu Gly Lys Lys Leu Gly Ile Pro Arg Gly 205 210 215	976
GTA CAA AGG GAC ACC ATG TGG CGG ATC TTT ACT GGA TCG CTG CTG GTA Val Gln Arg Asp Thr Met Trp Arg Ile Phe Thr Gly Ser Leu Leu Val 220 225 230	1024
GAG GAG AAG TCA AGT GCC CTT CTG CAT GAC CTT CGA GAG ATT GAG GCC Glu Glu Lys Ser Ser Ala Leu Leu His Asp Leu Arg Glu Ile Glu Ala 235 240 245	1072
TGG ATC TAT CGA TTG CTG CGC TCC CCA GTA CCC GTC TCT GGG CAG AAG Trp Ile Tyr Arg Leu Leu Arg Ser Pro Val Pro Val Ser Gly Gln Lys 250 255 260 265	1120
CGA GTA GAC ATC GAG GTC CTA CCC CAA GAG CTC CAG CCA GCT CTG ACC Arg Val Asp Ile Glu Val Leu Pro Gln Glu Leu Gln Pro Ala Leu Thr 270 275 280	1168
TTT GCT CTT CCA GAC CCA TCT CGA TTC ACC CTA GTG GAT TTC CCA CTG Phe Ala Leu Pro Asp Pro Ser Arg Phe Thr Leu Val Asp Phe Pro Leu 285 290 295	1216
CAC CTT CCC TTG GAA CTT CTA GGT GTG GAC GCC TGT CTC CAG GTG CTA His Leu Pro Leu Glu Leu Leu Gly Val Asp Ala Cys Leu Gln Val Leu 300 305 310	1264
ACC TGC ATT CTG TTA GAG CAC AAG GTG GTG CTA CAG TCC CGA GAC TAC Thr Cys Ile Leu Leu Glu His Lys Val Val Leu Gln Ser Arg Asp Tyr 315 320 325	1312
AAT GCA CTC TCC ATG TCT GTG ATG GCA TTC GTG GCA ATG ATC TAC CCA Asn Ala Leu Ser Met Ser Val Met Ala Phe Val Ala Met Ile Tyr Pro 330 335 340 345	1360
CTG GAA TAT ATG TTT CCT GTC ATC CCG CTG CTA CCC ACC TGC ATG GCA Leu Glu Tyr Met Phe Pro Val Ile Pro Leu Leu Pro Thr Cys Met Ala 350 355 360	1408
TCA GCA GAG CAG CTG CTG TTG GCT CCA ACC CCG TAC ATC ATT GGG GTT Ser Ala Glu Gln Leu Leu Ala Pro Thr Pro Tyr Ile Ile Gly Val 365 370 375	1456
CCT GCC AGC TTC TTC CTC TAC AAA CTG GAC TTC AAA ATG CCT GAT GAT Pro Ala Ser Phe Phe Leu Tyr Lys Leu Asp Phe Lys Met Pro Asp Asp 380 385 390	1504
GTA TGG CTA GTG GAT CTG GAC AGC AAT AGG GTG ATT GCC CCC ACC AAT Val Trp Leu Val Asp Leu Asp Ser Asn Arg Val Ile Ala Pro Thr Asn 395 400 405	1552
GCA GAA GTG CTG CCT ATC CTG CCA GAA CCA GAA TCA CTA GAG CTG AAA Ala Glu Val Leu Pro Ile Leu Pro Glu Pro Glu Ser Leu Glu Leu Lys 410 415 420 425	1600

AAG CAT TTA AAG CAG GCC TTG GCC AGC ATG AGT CTC AAC ACC CAG CCC Lys His Leu Lys Gln Ala Leu Ala Ser Met Ser Leu Asn Thr Gln Pro 430 435 440	1648
ATC CTC AAT CTG GAG AAA TTT CAT GAG GGC CAG GAG ATC CCC CTT CTC Ile Leu Asn Leu Glu Lys Phe His Glu Gly Gln Glu Ile Pro Leu Leu 445 450 455	1696
TTG GGA AGG CCT TCT AAT GAC CTG CAG TCC ACA CCG TCC ACT GAA TTC Leu Gly Arg Pro Ser Asn Asp Leu Gln Ser Thr Pro Ser Thr Glu Phe 460 465 470	1744
AAC CCA CTC ATC TAT GGC AAT GAT GTG GAT TCT GTG GAT GTT GCA ACC Asn Pro Leu Ile Tyr Gly Asn Asp Val Asp Ser Val Asp Val Ala Thr 475 480 485	1792
AGG GTT GCC ATG GTA CGG TTC TTC AAT TCC GCC AAC GTG CTG CAG GGA Arg Val Ala Met Val Arg Phe Asn Ser Ala Asn Val Leu Gln Gly 490 495 500 505	1840
TTT CAG ATG CAC ACG CGT ACC CTG CGC CTC TTT CCT CGG CCT GTG GTA Phe Gln Met His Thr Arg Thr Leu Arg Leu Phe Pro Arg Pro Val Val 510 515 520	1888
GCT TTT CAA GCT GGC TCC TTT CTA GCC TCA CGT CCC CGG CAG ACT CCT Ala Phe Gln Ala Gly Ser Phe Leu Ala Ser Arg Pro Arg Gln Thr Pro 525 530 535	1936
TTT GCC GAG AAA TTG GCC AGG ACT CAG GCT GTG GAG TAC TTT GGG GAA Phe Ala Glu Lys Leu Ala Arg Thr Gln Ala Val Glu Tyr Phe Gly Glu 540 545 550	1984
TGG ATC CTT AAC CCC ACC AAC TAT GCC TTT CAG CGA ATT CAC AAC AAT Trp Ile Leu Asn Pro Thr Asn Tyr Ala Phe Gln Arg Ile His Asn Asn 555 560 565	2032
ATG TTT GAT CCA GCC CTG ATT GGT GAC AAG CCA AAG TGG TAT GCT CAT Met Phe Asp Pro Ala Leu Ile Gly Asp Lys Pro Lys Trp Tyr Ala His 570 575 580 585	2080
CAG CTG CAG CCT ATC CAC TAT CGC GTC TAT GAC AGC AAT TCC CAG CTG Gln Leu Gln Pro Ile His Tyr Arg Val Tyr Asp Ser Asn Ser Gln Leu 590 595 600	2128
GCT GAG GCC CTG AGT GTA CCA CCA GAG CGG GAC TCT GAC TCC GAA CCT Ala Glu Ala Leu Ser Val Pro Pro Glu Arg Asp Ser Asp Ser Glu Pro 605 610 615	2176
ACT GAT GAT AGT GGC AGT GAT ATG GAT TAT GAC GAT TCA AGC TCT Thr Asp Asp Ser Gly Ser Asp Ser Met Asp Tyr Asp Asp Ser Ser Ser 620 625 630	2224
TCT TAC TCC TCC CTT GGT GAC TTT GTC AGT GAA ATG ATG AAA TGT GAC Ser Tyr Ser Ser Leu Glu Asp Phe Val Ser Glu Met Met Lys Cys Asp 635 640 645	2272
ATT AAT GGT GAT ACT CCC AAT GTG GAC CCT CTG ACA CAT GCA GCA CTG Ile Asn Gly Asp Thr Pro Asn Val Asp Pro Leu Thr His Ala Ala Leu 650 655 660 665	2320
GGG GAT GCC AGC GAG GTG GAG ATT GAC GAG CTG CAG AAT CAG AAG GAA Gly Asp Ala Ser Glu Val Glu Ile Asp Glu Leu Gln Asn Gln Lys Glu 670 675 680	2368
GCA GAA GAG CCT GGC CCA GAC AGT GAG AAC TCT CAG GAA AAC CCC CCA Ala Glu Glu Pro Gly Pro Asp Ser Glu Asn Ser Gln Glu Asn Pro Pro 685 690 695	2416

CTG CGC TCC AGC TCT AGC ACC ACA GCC AGC AGC AGC CCC AGC ACT GTC Leu Arg Ser Ser Ser Ser Thr Thr Ala Ser Ser Ser Pro Ser Thr Val 700 705 710	2464
ATC CAC GGA GCC AAC TCT GAA CCT GCT GAC TCT ACG GAG ATG GAT GAT Ile His Gly Ala Asn Ser Glu Pro Ala Asp Ser Thr Glu Met Asp Asp 715 720 725	2512
AAG GCA GCA GTA GGC GTC TCC AAG CCC CTC CCT TCC GTG CCT CCC AGC Lys Ala Ala Val Gly Val Ser Lys Pro Leu Pro Ser Val Pro Pro Ser 730 735 740 745	2560
ATT GGC AAA TCG AAC ATG GAC AGA CGT CAG GCA GAA ATT GGA GAG GGG Ile Gly Lys Ser Asn Met Asp Arg Arg Gln Ala Glu Ile Gly Glu Gly 750 755 760	2608
TCA GTG CGC CGG CGA ATC TAT GAC AAT CCA TAC TTC GAG CCC CAA TAT Ser Val Arg Arg Ile Tyr Asp Asn Pro Tyr Phe Glu Pro Gln Tyr 765 770 775	2656
GGC TTT CCC CCT GAG GAA GAT GAG GAT GAG CAG GGG GAA AGT TAC ACT Gly Phe Pro Pro Glu Glu Asp Glu Asp Glu Gln Gly Glu Ser Tyr Thr 780 785 790	2704
CCC CGA TTC AGC CAA CAT GTC AGT GGC AAT CGG GCT CAA AAG CTG CTG Pro Arg Phe Ser Gln His Val Ser Gly Asn Arg Ala Gln Lys Leu Leu 795 800 805	2752
CGG CCC AAC AGC TTG AGA CTG GCA AGT GAC TCA GAT GCA GAG TCA GAC Arg Pro Asn Ser Leu Arg Leu Ala Ser Asp Ser Asp Ala Glu Ser Asp 810 815 820 825	2800
TCT CGG GCA AGC TCT CCC AAC TCC ACC GTC TCC AAC ACC AGC ACC GAG Ser Arg Ala Ser Ser Pro Asn Ser Thr Val Ser Asn Thr Ser Thr Glu 830 835 840	2848
GGC TTC GGG GGC ATC ATG TCT TTT GCC AGC AGC CTC TAT CGG AAC CAC Gly Phe Gly Gly Ile Met Ser Phe Ala Ser Ser Leu Tyr Arg Asn His 845 850 855	2896
AGT ACC AGC TTC AGT CTT TCA AAC CTC ACA CTG CCC ACC AAA GGT GCC Ser Thr Ser Phe Ser Leu Ser Asn Leu Thr Leu Pro Thr Lys Gly Ala 860 865 870	2944
CGA GAG AAG GCC ACG CCC TTC CCC AGT CTG AAA GGA AAC AGG AGG GCG Arg Glu Lys Ala Thr Pro Phe Pro Ser Leu Lys Gly Asn Arg Arg Ala 875 880 885	2992
TTA GTG GAT CAG AAG TCA TCT GTC ATT AAA CAC AGC CCA ACA GTG AAA Leu Val Asp Gln Lys Ser Ser Val Ile Lys His Ser Pro Thr Val Lys 890 895 900 905	3040
AGA GAA CCT CCA TCA CCC CAG GGT CGA TCC AGC AAT TCT AGT GAG AAC Arg Glu Pro Pro Ser Pro Gln Gly Arg Ser Ser Asn Ser Ser Glu Asn 910 915 920	3088
CAG CAG TTC CTG AAG GAG GTG GTG CAC AGC GTG CTG GAC GGC CAG GGA Gln Gln Phe Leu Lys Glu Val Val His Ser Val Leu Asp Gly Gln Gly 925 930 935	3136
GTT GGC TGG CTC AAC ATG AAA AAG GTG CGC CGG CTG CTG GAG AGC GAG Val Gly Trp Leu Asn Met Lys Lys Val Arg Arg Leu Leu Glu Ser Glu 940 945 950	3184
CAG CTG CGA GTC TTT GTC CTG AGC AAG CTG AAC CGC ATG GTG CAG TCA Gln Leu Arg Val Phe Val Leu Ser Lys Leu Asn Arg Met Val Gln Ser 955 960 965	3232

GAG GAC GAT GCC CGG CAG GAC ATC ATC CCG GAT GTG GAG ATC AGT CGG Glu Asp Asp Ala Arg Gln Asp Ile Ile Pro Asp Val Glu Ile Ser Arg 970 975 980 985	3280
AAG GTG TAC AAG GGA ATG TTA GAC CTC CTC AAG TGT ACA GTC CTC AGC Lys Val Tyr Lys Gly Met Leu Asp Leu Leu Lys Cys Thr Val Leu Ser 990 995 1000	3328
TTG GAG CAG TCC TAT GCC CAC GCG GGT CTG GGT GGC ATG GCC AGC ATC Leu Glu Gln Ser Tyr Ala His Ala Gly Leu Gly Gly Met Ala Ser Ile 1005 1010 1015	3376
TTT GGG CTT TTG GAG ATT GCC CAG ACC CAC TAC TAT AGT AAA GAA CCA Phe Gly Leu Leu Glu Ile Ala Gln Thr His Tyr Ser Lys Glu Pro 1020 1025 1030	3424
GAC AAG CGG AAG AGA AGT CCA ACA GAA AGT GTA AAT ACC CCA GTT GGC Asp Lys Arg Lys Arg Ser Pro Thr Glu Ser Val Asn Thr Pro Val Gly 1035 1040 1045	3472
AAG GAT CCT GGC CTA GCT GGG CGG GGG GAC CCA AAG GCT ATG GCA CAA Lys Asp Pro Gly Leu Ala Gly Arg Gly Asp Pro Lys Ala Met Ala Gln 1050 1055 1060 1065	3520
CTG AGA GTT CCA CAA CTG GGA CCT CGG GCA CCA AGT GCC ACA GGA AAG Leu Arg Val Pro Gln Leu Gly Pro Arg Ala Pro Ser Ala Thr Gly Lys 1070 1075 1080	3568
GGT CCT AAG GAA CTG GAC ACC AGA AGT TTA AAG GAA GAA AAT TTT ATA Gly Pro Lys Glu Leu Asp Thr Arg Ser Leu Lys Glu Glu Asn Phe Ile 1085 1090 1095	3616
GCA TCT ATT GGG CCT GAA GTA ATC AAA CCT GTC TTT GAC CTT GGT GAG Ala Ser Ile Gly Pro Glu Val Ile Lys Pro Val Phe Asp Leu Gly Glu 1100 1105 1110	3664
ACA GAG GAG AAA AAG TCC CAG ATC AGC GCA GAC AGT GGT GTG AGC CTG Thr Glu Glu Lys Ser Gln Ile Ser Ala Asp Ser Gly Val Ser Leu 1115 1120 1125	3712
ACG TCT AGT TCC CAG AGG ACT GAT CAA GAC TCT GTC ATC GGC GTG AGT Thr Ser Ser Ser Gln Arg Thr Asp Gln Asp Ser Val Ile Gly Val Ser 1130 1135 1140 1145	3760
CCA GCT GTT ATG ATC CGC AGC TCA AGT CAG GAT TCT GAA GTT AGC ACC Pro Ala Val Met Ile Arg Ser Ser Gln Asp Ser Glu Val Ser Thr 1150 1155 1160	3808
GTG GTG AGT AAT AGC TCT GGA GAG ACC CTT GGA GCT GAC AGT GAC TTG Val Val Ser Asn Ser Ser Gly Glu Thr Leu Gly Ala Asp Ser Asp Leu 1165 1170 1175	3856
AGC AGC AAT GCA GGT GAT GGA CCA GGT GGC GAG GGC AGT GTT CAC CTG Ser Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly Ser Val His Leu 1180 1185 1190	3904
GCA AGC TCT CGG GGC ACT TTG TCT GAT AGT GAA ATT GAG ACC AAC TCT Ala Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile Glu Thr Asn Ser 1195 1200 1205	3952
GCC ACA AGC ACC ATC TTT GGT AAA GCC CAC AGC TTG AAG CCA AGC ATA Ala Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile 1210 1215 1220 1225	4000
AAG GAG AAG CTG GCA GGC AGC CCC ATT CGT ACT TCT GAA GAT GTG AGC Lys Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser 1230 1235 1240	4048

09086356 4420074

CAG CGA GTC TAT CTC TAT GAG GGA CTC CTA GGC AAA GAG CGT TCT ACT Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr 1245 1250 1255	4096
TTA TGG GAC CAA ATG CAA TTC TGG GAA GAT GCC TTC TTA GAT GCT GTG Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val 1260 1265 1270	4144
ATG TTG GAG AGA GAA GGG ATG GGT ATG GAC CAG GGT CCC CAG GAA ATG Met Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met 1275 1280 1285	4192
ATC GAC AGG TAC CTG TCC CTT GGA GAA CAT GAC CGG AAG CGC CTG GAA Ile Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu 1290 1295 1300 1305	4240
GAT GAT GAA GAT CGC TTG CTG GCC ACA CTT CTG CAC AAC CTC ATC TCC Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser 1310 1315 1320	4288
TAC ATG CTG CTG ATG AAG GTA AAT AAG AAT GAC ATC CGC AAG AAG GTG Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val 1325 1330 1335	4336
AGG CGC CTA ATG GGA AAG TCG CAC ATT GGG CTT GTG TAC AGC CAG CAA Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln 1340 1345 1350	4384
ATC AAT GAG GTG CTT GAT CAG CTG GCG AAC CTG AAT GGA CGC GAT CTC Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu 1355 1360 1365	4432
TCT ATC TGG TCC AGT GGC AGC CGG CAC ATG AAG AAG CAG ACA TTT GTG Ser Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val 1370 1375 1380 1385	4480
GTA CAT GCA GGG ACA GAT ACA AAC GGA GAT ATC TTT TTC ATG GAG GTG Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val 1390 1395 1400	4528
TGC GAT GAC TGT GTG TTG CGT AGT AAC ATC GGA ACA GTG TAT GAG Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu 1405 1410 1415	4576
CGC TGG TGG TAC GAG AAG CTC ATC AAC ATG ACC TAC TGT CCC AAG ACG Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr 1420 1425 1430	4624
AAG GTG TTG TGC TTG TGG CGT AGA AAT GGC TCT GAG ACC CAG CTC AAC Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn 1435 1440 1445	4672
AAG TTC TAT ACT AAA AAG TGT CGG GAG CTG TAC TAC TGT GTG AAG GAC Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp 1450 1455 1460 1465	4720
AGC ATG GAG CGC GCT GCC CGA CAG CAA AGC ATC AAA CCC GGA CCT Ser Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro 1470 1475 1480	4768
GAA TTG GGT GGC GAG TTC CCT GTG CAG GAC CTG AAG ACT GGT GAG GGT Glu Leu Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly 1485 1490 1495	4816
GGC CTG CTG CAG GTG ACC CTG GAA GGG ATC AAC CTC AAA TTC ATG CAC Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His 1500 1505 1510	4864

Sequence Report

AAT CAG GTT TTC ATA GAG CTG AAT CAC ATT AAA AAG TGC AAT ACA GTT	4912
Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val	
1515 1520 1525	
CGA GGC GTC TTT GTC CTG GAG GAA TTT GTT CCT GAA ATT AAA GAA GTG	4960
Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val	
1530 1535 1540 1545	
GTG AGC CAC AAG TAC AAG ACA CCA ATG GCC CAC GAA ATC TGC TAC TCC	5008
Val Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser	
1550 1555 1560	
GTA TTA TGT CTC TTC TCG TAC GTG GCT GCA GTT CAT AGC AGT GAG GAA	5056
Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu	
1565 1570 1575	
GAT CTC AGA ACC CCG CCC CGG CCT GTC TCT AGC TGA TGGAGAGGGG	5102
Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser *	
1580 1585	
CTACGCAGCT GCCCCAGCCC AGGGCACGCC CCTGGCCCT TGCTGTTCCC AAGTGCACGA	5162
TGCTGCTGTG ACTGAGGAGT GGATGATGCT CGTGTGTCCCT CTGCAAGCCC CCTGCTGTGG	5222
CTTGGTTGGT TACCGTTAT GTGTCCCTCT GAGTGTGTCT TGAGCGTGTC CACCTCTCC	5282
CTCTCCACTC CCAGAAGACC AAACTGCCCT CCCCTCAGGG CTCAAGAATG TGTACAGTCT	5342
GTGGGGCCGG TGTGAACCCA CTATTTGTG TCCTTGAGAC ATTTGTGTTG TGGTTCCCTTG	5402
TCCTTGTCCTC TGGCGTTATA ACTGTCCACT GCAAGAGTCT GGCTCTCCCT TCTCTGTGAC	5462
CCGGCATGAC TGGGCGCCTG GAGCAGTTTC ACTCTGTGAG GAGTGGAGGA ACCCTGGGC	5522
TCACCCCTCTC AGAGGAAGGG CACAGAGAGG AAGGGAAGAA TTGGGGGGCA GCCGGAGTGA	5582
GTGGCAGCCT CCCTGCTTCC TTCTGCATTC CCAAGCCGGC AGCTACTGCC CAGGGCCCGC	5642
AGTGTGGCT GCTGCCTGCC ACAGCCTCTG TGACTGCAGT GGAGCGGCCGA ATTCCCTGTG	5702
GCCTGCCACG CCTTCGGCAT CAGAGGATGG AGTGGTCGAG GCTAGTGGAG TCCCAGGGAC	5762
CGCTGGCTGC TCTGCCTGAG CATCAGGGAG GGGCAGGAA AGACCAAGCT GGGTTTGCAC	5822
ATCTGTCTGC AGGCTGTCTC TCCAGGCACG GGGTGTCAAG AGGGAGAGAC AGCCTGGGT	5882
TGGGCAAGAA ATGACTGTAA ATATTCAGC CCCACATTAT TTATAGAAAA TGTACAGTTG	5942
TGTGAATGTG AAATAAATGT CCTCAACTCC CAAAAAAA AAAAAAAA AAAAAAAA	6002

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1589 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val Gln Lys Lys Lys Phe Cys Pro Arg Leu Leu Asp Tyr Leu Val
1 5 10 15

Ile Val Gly Ala Arg His Pro Ser Ser Asp Ser Val Ala Gln Thr Pro

20

25

30

Glu Leu Leu Arg Arg Tyr Pro Leu Glu Asp His Thr Glu Phe Pro Leu
 35 40 45

Pro Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val
 50 55 60

Arg Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr
 65 70 75 80

Leu Thr Asp Lys Asp Thr Gly Val Thr Arg Tyr Gly Ile Cys Val Asn
 85 90 95

Phe Tyr Arg Ser Phe Gln Lys Arg Ile Ser Lys Glu Lys Gly Glu Gly
 100 105 110

Gly Ala Gly Ser Arg Gly Lys Glu Gly Thr His Ala Thr Cys Ala Ser
 115 120 125

Glu Glu Gly Gly Thr Glu Ser Ser Glu Ser Gly Ser Ser Leu Gln Pro
 130 135 140

Leu Ser Ala Asp Ser Thr Pro Asp Val Asn Gln Ser Pro Arg Gly Lys
 145 150 155 160

Arg Arg Ala Lys Ala Gly Ser Arg Ser Arg Asn Ser Thr Leu Thr Ser
 165 170 175

Leu Cys Val Leu Ser His Tyr Pro Phe Phe Ser Thr Phe Arg Glu Cys
 180 185 190

Leu Tyr Thr Leu Lys Arg Leu Val Asp Cys Cys Ser Glu Arg Leu Leu
 195 200 205

Gly Lys Lys Leu Gly Ile Pro Arg Gly Val Gln Arg Asp Thr Met Trp
 210 215 220

Arg Ile Phe Thr Gly Ser Leu Leu Val Glu Glu Lys Ser Ser Ala Leu
 225 230 235 240

Leu His Asp Leu Arg Glu Ile Glu Ala Trp Ile Tyr Arg Leu Leu Arg
 245 250 255

Ser Pro Val Pro Val Ser Gly Gln Lys Arg Val Asp Ile Glu Val Leu
 260 265 270

Pro Gln Glu Leu Gln Pro Ala Leu Thr Phe Ala Leu Pro Asp Pro Ser
 275 280 285

Arg Phe Thr Leu Val Asp Phe Pro Leu His Leu Pro Leu Glu Leu Leu
 290 295 300

Gly Val Asp Ala Cys Leu Gln Val Leu Thr Cys Ile Leu Leu Glu His
 305 310 315 320

Lys Val Val Leu Gln Ser Arg Asp Tyr Asn Ala Leu Ser Met Ser Val
 325 330 335

Met Ala Phe Val Ala Met Ile Tyr Pro Leu Glu Tyr Met Phe Pro Val
 340 345 350

Ile Pro Leu Leu Pro Thr Cys Met Ala Ser Ala Glu Gln Leu Leu Leu
 355 360 365

Ala Pro Thr Pro Tyr Ile Ile Gly Val Pro Ala Ser Phe Phe Leu Tyr
 370 375 380

Lys Leu Asp Phe Lys Met Pro Asp Asp Val Trp Leu Val Asp Leu Asp
385 390 395 400

Ser Asn Arg Val Ile Ala Pro Thr Asn Ala Glu Val Leu Pro Ile Leu
405 410 415

Pro Glu Pro Glu Ser Leu Glu Leu Lys Lys His Leu Lys Gln Ala Leu
420 425 430

Ala Ser Met Ser Leu Asn Thr Gln Pro Ile Leu Asn Leu Glu Lys Phe
435 440 445

His Glu Gly Gln Glu Ile Pro Leu Leu Leu Gly Arg Pro Ser Asn Asp
450 455 460

Leu Gln Ser Thr Pro Ser Thr Glu Phe Asn Pro Leu Ile Tyr Gly Asn
465 470 475 480

Asp Val Asp Ser Val Asp Val Ala Thr Arg Val Ala Met Val Arg Phe
485 490 495

Phe Asn Ser Ala Asn Val Leu Gln Gly Phe Gln Met His Thr Arg Thr
500 505 510

Leu Arg Leu Phe Pro Arg Pro Val Val Ala Phe Gln Ala Gly Ser Phe
515 520 525

Leu Ala Ser Arg Pro Arg Gln Thr Pro Phe Ala Glu Lys Leu Ala Arg
530 535 540

Thr Gln Ala Val Glu Tyr Phe Gly Glu Trp Ile Leu Asn Pro Thr Asn
545 550 555 560

Tyr Ala Phe Gln Arg Ile His Asn Asn Met Phe Asp Pro Ala Leu Ile
565 570 575

Gly Asp Lys Pro Lys Trp Tyr Ala His Gln Leu Gln Pro Ile His Tyr
580 585 590

Arg Val Tyr Asp Ser Asn Ser Gln Leu Ala Glu Ala Leu Ser Val Pro
595 600 605

Pro Glu Arg Asp Ser Asp Ser Glu Pro Thr Asp Asp Ser Gly Ser Asp
610 615 620

Ser Met Asp Tyr Asp Asp Ser Ser Ser Ser Tyr Ser Ser Leu Gly Asp
625 630 635 640

Phe Val Ser Glu Met Met Lys Cys Asp Ile Asn Gly Asp Thr Pro Asn
645 650 655

Val Asp Pro Leu Thr His Ala Ala Leu Gly Asp Ala Ser Glu Val Glu
660 665 670

Ile Asp Glu Leu Gln Asn Gln Lys Glu Ala Glu Glu Pro Gly Pro Asp
675 680 685

Ser Glu Asn Ser Gln Glu Asn Pro Pro Leu Arg Ser Ser Ser Ser Thr
690 695 700

Thr Ala Ser Ser Ser Pro Ser Thr Val Ile His Gly Ala Asn Ser Glu
705 710 715 720

Pro Ala Asp Ser Thr Glu Met Asp Asp Lys Ala Ala Val Gly Val Ser
725 730 735

Lys Pro Leu Pro Ser Val Pro Pro Ser Ile Gly Lys Ser Asn Met Asp

740 745 750

Arg Arg Gln Ala Glu Ile Gly Glu Gly Ser Val Arg Arg Arg Ile Tyr
 755 760 765

Asp Asn Pro Tyr Phe Glu Pro Gln Tyr Gly Phe Pro Pro Glu Glu Asp
 770 775 780

Glu Asp Glu Gln Gly Glu Ser Tyr Thr Pro Arg Phe Ser Gln His Val
 785 790 795 800

Ser Gly Asn Arg Ala Gln Lys Leu Leu Arg Pro Asn Ser Leu Arg Leu
 805 810 815

Ala Ser Asp Ser Asp Ala Glu Ser Asp Ser Arg Ala Ser Ser Pro Asn
 820 825 830

Ser Thr Val Ser Asn Thr Ser Thr Glu Gly Phe Gly Gly Ile Met Ser
 835 840 845

Phe Ala Ser Ser Leu Tyr Arg Asn His Ser Thr Ser Phe Ser Leu Ser
 850 855 860

Asn Leu Thr Leu Pro Thr Lys Gly Ala Arg Glu Lys Ala Thr Pro Phe
 865 870 875 880

Pro Ser Leu Lys Gly Asn Arg Arg Ala Leu Val Asp Gln Lys Ser Ser
 885 890 895

Val Ile Lys His Ser Pro Thr Val Lys Arg Glu Pro Pro Ser Pro Gln
 900 905 910

Gly Arg Ser Ser Asn Ser Ser Glu Asn Gln Gln Phe Leu Lys Glu Val
 915 920 925

Val His Ser Val Leu Asp Gly Gln Gly Val Gly Trp Leu Asn Met Lys
 930 935 940

Lys Val Arg Arg Leu Leu Glu Ser Glu Gln Leu Arg Val Phe Val Leu
 945 950 955 960

Ser Lys Leu Asn Arg Met Val Gln Ser Glu Asp Asp Ala Arg Gln Asp
 965 970 975

Ile Ile Pro Asp Val Glu Ile Ser Arg Lys Val Tyr Lys Gly Met Leu
 980 985 990

Asp Leu Leu Lys Cys Thr Val Leu Ser Leu Glu Gln Ser Tyr Ala His
 995 1000 1005

Ala Gly Leu Gly Gly Met Ala Ser Ile Phe Gly Leu Leu Glu Ile Ala
 1010 1015 1020

Gln Thr His Tyr Tyr Ser Lys Glu Pro Asp Lys Arg Lys Arg Ser Pro
 1025 1030 1035 1040

Thr Glu Ser Val Asn Thr Pro Val Gly Lys Asp Pro Gly Leu Ala Gly
 1045 1050 1055

Arg Gly Asp Pro Lys Ala Met Ala Gln Leu Arg Val Pro Gln Leu Gly
 1060 1065 1070

Pro Arg Ala Pro Ser Ala Thr Gly Lys Gly Pro Lys Glu Leu Asp Thr
 1075 1080 1085

Arg Ser Leu Lys Glu Glu Asn Phe Ile Ala Ser Ile Gly Pro Glu Val
 1090 1095 1100

Ile Lys Pro Val Phe Asp Leu Gly Glu Thr Glu Glu Lys Lys Ser Gln
 1105 1110 1115 1120
 Ile Ser Ala Asp Ser Gly Val Ser Leu Thr Ser Ser Ser Gln Arg Thr
 1125 1130 1135
 Asp Gln Asp Ser Val Ile Gly Val Ser Pro Ala Val Met Ile Arg Ser
 1140 1145 1150
 Ser Ser Gln Asp Ser Glu Val Ser Thr Val Val Ser Asn Ser Ser Gly
 1155 1160 1165
 Glu Thr Leu Gly Ala Asp Ser Asp Leu Ser Ser Asn Ala Gly Asp Gly
 1170 1175 1180
 Pro Gly Gly Glu Gly Ser Val His Leu Ala Ser Ser Arg Gly Thr Leu
 1185 1190 1195 1200
 Ser Asp Ser Glu Ile Glu Thr Asn Ser Ala Thr Ser Thr Ile Phe Gly
 1205 1210 1215
 Lys Ala His Ser Leu Lys Pro Ser Ile Lys Glu Lys Leu Ala Gly Ser
 1220 1225 1230
 Pro Ile Arg Thr Ser Glu Asp Val Ser Gln Arg Val Tyr Leu Tyr Glu
 1235 1240 1245
 Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu Trp Asp Gln Met Gln Phe
 1250 1255 1260
 Trp Glu Asp Ala Phe Leu Asp Ala Val Met Leu Glu Arg Glu Gly Met
 1265 1270 1275 1280
 Gly Met Asp Gln Gly Pro Gln Glu Met Ile Asp Arg Tyr Leu Ser Leu
 1285 1290 1295
 Gly Glu His Asp Arg Lys Arg Leu Glu Asp Asp Glu Asp Arg Leu Leu
 1300 1305 1310
 Ala Thr Leu Leu His Asn Leu Ile Ser Tyr Met Leu Leu Met Lys Val
 1315 1320 1325
 Asn Lys Asn Asp Ile Arg Lys Lys Val Arg Arg Leu Met Gly Lys Ser
 1330 1335 1340
 His Ile Gly Leu Val Tyr Ser Gln Gln Ile Asn Glu Val Leu Asp Gln
 1345 1350 1355 1360
 Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser Ile Trp Ser Ser Gly Ser
 1365 1370 1375
 Arg His Met Lys Lys Gln Thr Phe Val Val His Ala Gly Thr Asp Thr
 1380 1385 1390
 Asn Gly Asp Ile Phe Phe Met Glu Val Cys Asp Asp Cys Val Val Leu
 1395 1400 1405
 Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg Trp Trp Tyr Glu Lys Leu
 1410 1415 1420
 Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys Val Leu Cys Leu Trp Arg
 1425 1430 1435 1440
 Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys Phe Tyr Thr Lys Lys Cys
 1445 1450 1455
 Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser Met Glu Arg Ala Ala Ala

1460 1465 1470

Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu Leu Gly Gly Glu Phe Pro
 1475 1480 1485

Val Gln Asp Leu Lys Thr Gly Glu Gly Gly Leu Leu Gln Val Thr Leu
 1490 1495 1500

Glu Gly Ile Asn Leu Lys Phe Met His Asn Gln Val Phe Ile Glu Leu -
 1505 1510 1515 1520

Asn His Ile Lys Lys Cys Asn Thr Val Arg Gly Val Phe Val Leu Glu
 1525 1530 1535

Glu Phe Val Pro Glu Ile Lys Glu Val Val Ser His Lys Tyr Lys Thr
 1540 1545 1550

Pro Met Ala His Glu Ile Cys Tyr Ser Val Leu Cys Leu Phe Ser Tyr
 1555 1560 1565

Val Ala Ala Val His Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg
 1570 1575 1580

Pro Val Ser Ser *
 1585

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGACGAGGA GACATGGCGG CGGCGCCGGT AGCGGCTGGG TCTGGAGCCG GCCGAGGGAG	60
ACGGTCGGCA GCCACAGTGG CGGCTTGGGG CGGATGGGGC GGCGGGCCGC GGCCTGGTAA	120
CATTCTGCTG CAGCTGCCGC AGGGCCAGCT GACCAGCCGG GGCCCTGGTCC GGGCGGTGCA	180
GTTCACTGAG ACTTTTTGA CGGAGAGGGA CAAACAATCC AAGTGGAGTG GAATTCCCTCA	240
GCTGCTCCTC AAGCTGCACA CCACCAAGCCA CCTCCACAGT GACTTTGTTG AGTGTCAAAA	300
CATCCTCAAG GAAATTCTC CTCTTCTCTC CATGGAGGCT ATGGCATTG TTACTGAAGA	360
GAGGAAACTT ACCCAAGAAA CCACTTATCC AAATACTTAC ATTTTGACT TGTTGGAGG	420
TGTTGATCTT CTTGTAGAAA TTCTTATGAG GCCTACGATC TCTATCCGGG GACAGAAACT	480
GAAAATAAGT GATGAAATGT CCAAGGACTG CTTGAGTATC CTGTATAATA CCTGTGTCTG	540
TACAGAGGGA GTTACAAAGC GTTGGCAGA AAAGAATGAC TTTGTGATCT TCCTGTTAC	600
ATTGATGACA AGTAAGAAGA CATTCTTACA AACAGCAACC CTCATTGAAG ATATTTAGG	660

TGTTAAAAAG GAAATGATCC GACTAGATGA AGTCCCCAAT CTGAGTTCT TAGTATCAA	720
TTTCGATCAG CAGCAGCTCG CTAATTTCTG CGGGATTCTG GCTGTCACCA TTTCAGAGAT	780
GGATACAGGG AATGATGACA AGCACACGCT TCTTGCCAAA AATGCTCAAC AGAAGAAGAG	840
CTTGAGTTTG GGGCCTTCTG CAGCTGAAAT CAATCAAGCG GCCCTCTCA GCATTCTGG	900
CTTTGTTGAG CGGCTTGCA AACTGGCGAC TCGAAAGGTG TCAGAGTCAA CGGGCACAGE	960
CAGCTCCTT CAGGAGTTGG AAGAGTGGTA CACATGGCTA GACAATGCTT TGGTGCTAGA	1020
TGCCCTGATG CGAGTGGCCA ATGAGGAGTC AGAGCACAAT CAAGCCTCCA TTGTGTTCCC	1080
TCCTCCAGGG GCTTCTGAGG AGAATGGCCT GCCTCACACG TCAGCCAGAA CCCAGCTGCC	1140
CCAGTCAATG AAGATTATGC ATGAGATCAT GTACAAACTG GAAGTGCTCT ATGTCCTCTG	1200
CGTGCTGCTG ATGGGGCGTC AGCGAAACCA GGTTCACAGA ATGATTGCAG AGTTCAAGCT	1260
GATCCCTGGA CTTAATAATT TGTTTGACAA ACTGATTGG AGGAAGCATT CAGCATCTGC	1320
CCTTGTCTC CATGGTCACA ACCAGAACTG TGACTGTAGC CCGGACATCA CCTTGAAGAT	1380
ACAGTTTTG AGGCTTCTTC AGAGCTTCAG TGACCACCAC GAGAACAAAGT ACTTGTACT	1440
CAACAACCAG GAGCTGAATG AACTCAGTGC CATCTCTCTC AAGGCCAAC A TCCCTGAGGT	1500
GGAAGCTGTC CTCAACACCG ACAGGAGTTT GGTGTGTGAT GGGAAAGAGGG GCTTATTAAC	1560
TCGTCTGCTG CAGGTCAATGA AGAAGGAGCC AGCAGAGTCG TCTTCAGGT TTTGGCAAGC	1620
TCGGGCTGTG GAGAGTTCC TCCGAGGGAC CACCTCTTAT GCAGACCAGA TGTTCTGCT	1680
GAAGCGAGGC CTCTTGGAGC ACATCCTTTA CTGCATTGTG GACAGCGAGT GTAAGTCAAG	1740
GGATGTGCTC CAGAGTTACT TTGACCTCCT GGGGGAGCTG ATGAAGTTCA ACGTTGATGC	1800
ATTCAAGAGA TTCAATAAAA ATATCAACAC CGATGCAAAG TTCCAGGTAT TCCTGAAGCA	1860
GATCAACAGC TCCCTGGTGG ACTCCAACAT GCTGGTGCAGC TGTGTCACTC TGTCCCTGGA	1920
CCGATTGAA AACCAAGGTGG ATATGAAAGT TGCCGAGGTA CTGCTGAAT GCCGCCTGCT	1980
CGCCTACATA TCCCAGGTGC CCACGCAGAT GTCTTCTCTC TTCCGCCTCA TCAACATCAT	2040
CCACGTGCAG ACGCTGACCC AGGAGAACGT CAGCTGCCTC AACACCAGCC TGGTGATCCT	2100
GATGCTGGCC CGACGGAAAG AGCGGCTGCC CCTGTACCTG CGGCTGCTGC AGCGGATGGA	2160
GCACAGCAAG AAGTACCCCG GCTTCCTGCT CAACAACCTTC CACAACCTGC TGCGCTTCTG	2220
GCAGCAGCAC TACCTGCACA AGGACAAGGA CAGCACCTGC CTAGAGAACAA GCTCCTGCAT	2280
CAGCTTCTCA TACTGGAAGG AGACAGTGTC CATCCTGTTG AACCCGGACC GGCAGTCACC	2340
CTCTGCTCTC GTTAGCTACA TTGAGGAGCC CTACATGGAC ATAGACAGGG ACTTCACTGA	2400
GGAGTGACCT TGGGCCAGGC CTCGGGAGGC TGCTGGGCCA GTGTGGGTGA GCGTGGGTAC	2460
GATGCCACAC GCC	2473

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 797 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Ala Ala Pro Val Ala Ala Gly Ser Gly Ala Gly Arg Gly Arg
1 5 10 15

Arg Ser Ala Ala Thr Val Ala Ala Trp Gly Gly Trp Gly Gly Arg Pro
20 25 30

Arg Pro Gly Asn Ile Leu Leu Gln Leu Arg Gln Gly Gln Leu Thr Gly
35 40 45

Arg Gly Leu Val Arg Ala Val Gln Phe Thr Glu Thr Phe Leu Thr Glu
50 55 60

Arg Asp Lys Gln Ser Lys Trp Ser Gly Ile Pro Gln Leu Leu Leu Lys
65 70 75 80

Leu His Thr Thr Ser His Leu His Ser Asp Phe Val Glu Cys Gln Asn
85 90 95

Ile Leu Lys Glu Ile Ser Pro Leu Leu Ser Met Glu Ala Met Ala Phe
100 105 110

Val Thr Glu Glu Arg Lys Leu Thr Gln Glu Thr Thr Tyr Pro Asn Thr
115 120 125

Tyr Ile Phe Asp Leu Phe Gly Val Asp Leu Leu Val Glu Ile Leu
130 135 140

Met Arg Pro Thr Ile Ser Ile Arg Gly Gln Lys Leu Lys Ile Ser Asp
145 150 155 160

Glu Met Ser Lys Asp Cys Leu Ser Ile Leu Tyr Asn Thr Cys Val Cys
165 170 175

Thr Glu Gly Val Thr Lys Arg Leu Ala Glu Lys Asn Asp Phe Val Ile
180 185 190

Phe Leu Phe Thr Leu Met Thr Ser Lys Lys Thr Phe Leu Gln Thr Ala
195 200 205

Thr Leu Ile Glu Asp Ile Leu Gly Val Lys Lys Glu Met Ile Arg Leu
210 215 220

Asp Glu Val Pro Asn Leu Ser Ser Leu Val Ser Asn Phe Asp Gln Gln
225 230 235 240

Gln Leu Ala Asn Phe Cys Arg Ile Leu Ala Val Thr Ile Ser Glu Met
245 250 255

Asp Thr Gly Asn Asp Asp Lys His Thr Leu Leu Ala Lys Asn Ala Gln
260 265 270

Gln Lys Lys Ser Leu Ser Leu Gly Pro Ser Ala Ala Glu Ile Asn Gln
275 280 285

Ala Ala Leu Leu Ser Ile Pro Gly Phe Val Glu Arg Leu Cys Lys Leu
290 295 300

Ala Thr Arg Lys Val Ser Glu Ser Thr Gly Thr Ala Ser Phe Leu Gln
 305 310 315 320
 Glu Leu Glu Glu Trp Tyr Thr Trp Leu Asp Asn Ala Leu Val Leu Asp
 325 330 335
 Ala Leu Met Arg Val Ala Asn Glu Ser Glu His Asn Gln Ala Ser
 340 345 350
 Ile Val Phe Pro Pro Pro Gly Ala Ser Glu Glu Asn Gly Leu Pro His
 355 360 365
 Thr Ser Ala Arg Thr Gln Leu Pro Gln Ser Met Lys Ile Met His Glu
 370 375 380
 Ile Met Tyr Lys Leu Glu Val Leu Tyr Val Leu Cys Val Leu Leu Met
 385 390 395 400
 Gly Arg Gln Arg Asn Gln Val His Arg Met Ile Ala Glu Phe Lys Leu
 405 410 415
 Ile Pro Gly Leu Asn Asn Leu Phe Asp Lys Leu Ile Trp Arg Lys His
 420 425 430
 Ser Ala Ser Ala Leu Val Leu His Gly His Asn Gln Asn Cys Asp Cys
 435 440 445
 Ser Pro Asp Ile Thr Leu Lys Ile Gln Phe Leu Arg Leu Leu Gln Ser
 450 455 460
 Phe Ser Asp His His Glu Asn Lys Tyr Leu Leu Leu Asn Asn Gln Glu
 465 470 475 480
 Leu Asn Glu Leu Ser Ala Ile Ser Leu Lys Ala Asn Ile Pro Glu Val
 485 490 495
 Glu Ala Val Leu Asn Thr Asp Arg Ser Leu Val Cys Asp Gly Lys Arg
 500 505 510
 Gly Leu Leu Thr Arg Leu Leu Gln Val Met Lys Lys Glu Pro Ala Glu
 515 520 525
 Ser Ser Phe Arg Phe Trp Gln Ala Arg Ala Val Glu Ser Phe Leu Arg
 530 535 540
 Gly Thr Thr Ser Tyr Ala Asp Gln Met Phe Leu Leu Lys Arg Gly Leu
 545 550 555 560
 Leu Glu His Ile Leu Tyr Cys Ile Val Asp Ser Glu Cys Lys Ser Arg
 565 570 575
 Asp Val Leu Gln Ser Tyr Phe Asp Leu Leu Gly Glu Leu Met Lys Phe
 580 585 590
 Asn Val Asp Ala Phe Lys Arg Phe Asn Lys Asn Ile Asn Thr Asp Ala
 595 600 605
 Lys Phe Gln Val Phe Leu Lys Gln Ile Asn Ser Ser Leu Val Asp Ser
 610 615 620
 Asn Met Leu Val Arg Cys Val Thr Leu Ser Leu Asp Arg Phe Glu Asn
 625 630 635 640
 Gln Val Asp Met Lys Val Ala Glu Val Leu Ser Glu Cys Arg Leu Leu
 645 650 655
 Ala Tyr Ile Ser Gln Val Pro Thr Gln Met Ser Phe Leu Phe Arg Leu

660

665

670

Ile Asn Ile Ile His Val Gln Thr Leu Thr Gln Glu Asn Val Ser Cys
675 680 685

Leu Asn Thr Ser Leu Val Ile Leu Met Leu Ala Arg Arg Lys Glu Arg
690 695 700

Leu Pro Leu Tyr Leu Arg Leu Leu Gln Arg Met Glu His Ser Lys Lys
705 710 715 720

Tyr Pro Gly Phe Leu Leu Asn Asn Phe His Asn Leu Leu Arg Phe Trp
725 730 735

Gln Gln His Tyr Leu His Lys Asp Lys Asp Ser Thr Cys Leu Glu Asn
740 745 750

Ser Ser Cys Ile Ser Phe Ser Tyr Trp Lys Glu Thr Val Ser Ile Leu
755 760 765

Leu Asn Pro Asp Arg Gln Ser Pro Ser Ala Leu Val Ser Tyr Ile Glu
770 775 780

Glu Pro Tyr Met Asp Ile Asp Arg Asp Phe Thr Glu Glu
785 790 795